

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:32:08 ; Search time 34.78 Seconds
(without alignments)
652.674 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543

Sequence: 1 MTEGDAISFAKDFLAGGIAAA.....LRGMAFVLVLYDELKKVI 298

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1 S03894	ADP, ATP carrier pr
2	1512	98.0	298	2 B43646	ADP, ATP carrier pr
3	1454	94.2	298	1 A29132	ADP, ATP carrier pr
4	1424	92.3	298	2 I60173	adenine nucleotide
5	1422	92.2	298	1 XMB0	ADP, ATP carrier pr
6	1418	91.9	298	2 S37210	ADP, ATP carrier pr
7	1409	91.3	298	1 A44778	ADP, ATP carrier pr
8	1405	91.1	298	2 S31814	ADP, ATP carrier pr
9	1184	76.7	301	1 S31935	ADP, ATP carrier pr
10	1041	67.5	313	2 T23207	hypothetical prote
11	1039	67.3	313	2 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP, ATP carrier pr
15	943	61.1	301	2 S51132	ADP, ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP, ATP carrier pr
17	772	50.0	308	1 S30259	ADP, ATP carrier pr
18	769	49.8	322	2 T40526	adp/atp translocas
19	768	49.8	386	2 T09709	ADP, ATP carrier pr
20	766	49.6	313	1 XWNC	ADP, ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP, ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP, ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP, ATP carrier pr
26	748	48.5	386	2 S21974	ADP, ATP carrier pr
27	747	48.4	306	2 T42011	ADP, ATP carrier pr
28	747	48.4	386	2 S17917	ADP, ATP carrier pr
29	744	48.2	387	2 S16568	ADP, ATP carrier pr

30	743	48.2	379	2 T04608	ADP, ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP, ATP carrier pr
32	742	48.1	382	2 S33630	ADP, ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP, ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP, ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP, ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP, ATP translocas
38	393	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	hypothetical prote
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	348	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

```
RESULT 1
S03894
ADP, ATP carrier protein T3 - human
N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #ext_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; M01D:89236396
A:Accession: S03894
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Altarid, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; M01D:88124845
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
A:Experimental source: liver
C:Gene: GDB:ANT3; ANT3Y
C:Genetics:
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2
C:Superfamily: ADP, ATP carrier protein, ADP, ATP carrier of sequences for GDB:ANT2
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP, ATP carrier protein repeat homology <MAY>
F:5-99/Domain: ADP, ATP carrier protein repeat homology <MAY>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <MAY>
F:207-298/Domain: ADP, ATP carrier protein repeat homology <MAY>

Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.3e-129;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 QY 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 298
 |||
 Db 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 298
 |||

RESULT 2

B43646.
 ADP,ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 4e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||
 Db 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||
 QY 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRFAAGNLASG 120
 |||
 Db 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRFAAGNLASG 120
 |||
 QY 121 GAAGATSLCFVPLDFARTRLADYKSGTEREFGDGLVYKIRKSDGIRGLYOGFSYS 180
 |||
 Db 121 GAAGATSLCFVPLDFARTRLADYKSGTEREFGDGLVYKIRKSDGIRGLYOGFSYS 180
 |||
 QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 QY 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 298
 |||
 Db 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 298
 |||

RESULT 3

A29132
 ADP,ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP,ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87166056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Waldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A24197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2P1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-q26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 5.4e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||
 Db 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||
 QY 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRFAAGNLASG 120
 |||
 Db 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRFAAGNLASG 120
 |||
 QY 121 GAAGATSLCFVPLDFARTRLADYKSGTEREFGDGLVYKIRKSDGIRGLYOGFSYS 180
 |||
 Db 121 GAAGATSLCFVPLDFARTRLADYKSGTEREFGDGLVYKIRKSDGIRGLYOGFSYS 180
 |||
 QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTVAAGVSPFDTVRRMM 240
 |||
 QY 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 296
 |||
 Db 241 QSGRGADIMYGTVCWKRIFRDEGKAFKFGANSNVLRGGAFAVLVLYDELKVI 296
 |||

RESULT 4

I60173
 adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shinozaki, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161
 A:Accession: I60173
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA3842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2.4e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

OY 1 MTEQASFAKPEFLAGGIAAATSKTAVPATIEPVTKLLLOYQHAKSRIADDKOVKGYVDDCVR 60
|||::|||||::|.....|.....|.....|.....|.....|.....|.....|.....|.....
Db 1 MGDAALSTLKDFLAGGIAAAVSATAVAPIERVKLLLLOQAHSKSKIASEKKGIIDCVR 60

OY 1 PKEGGVSEFMRGNLANVIARFYPTQALNFAEKDVKYKIIFLEGVDKHOFWFRPYFGANLASG 120
I PKGGGLSTFSMRGNLANVIARIRFPPTQALNFARKDKYKYKGFLEGGVDNRHQQFMRYEFGNLASG 120

Oy 121 GAAGATSISCFEVYPPLDEFARTRLADVGKSCTGEREFREGJGDCLVKITKSDGIRGLYQGFSVS 180
|||::|..|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|..
Db 121 GAACATSLSCFFVYPPLDEFATRRLAADVGKSSQREFNGIGDCILFKIFKSPDGKLGLYGQGSVS 180

Oy 181 VGGIIIVAAAEEGVYDPRAKGMLPDPKNHTIVSMNIQTOTAVAGVVSYPPDTYRRHRMM 240
181 VGGIIITRAAFEGYIDTAKGMLPDPKNHVITIISMAIOSYAVAGLVSYPPDYTRRRMM 240

Oy 241 QSGRGADIMVTGTVDCCRKFIREDEGRKAFFPKGMSNVLRMGGAFFVLVIDELCKKVY 298
|||::|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|..
Db 241 QSGRKGAIDIMVTGTVDCCWRKTAKDEGRKAFFPKGAMSNVLRMGGAFFVLVIDELIKTVV 298

RESULT 5
XMBIO
ADP, ATP carrier protein Tl - bovine
N: Alternate names: ADP/ATP translocase Tl
C: Species: Bos primigenius taurus (cattle)
C: Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C: Accession: A43646; A24822; A03181; A61343; S69369
C: Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A: Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A: Reference number: A43646; MUID: 89229093
A: Accession: A43646

A: Molecule type: mRNA
A: Residues: 1-298 <PM>
A: Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PID:g529415
R: Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A: Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A: Reference number: A24822; MUID: 86295775
A: Accession: A24822

A: Molecule type: mRNA
A: Residues: 208-298 <RAS>
A: Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
R: Aquila, H.; Mistra, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A: Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
A: Reference number: A03181; MUID: 82188267
A: Accession: A03181

A: Molecule type: Protein
A: Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AOU>
A: Note: residue 52 may be methyllysine
R: Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A: Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch
A: Reference number: A61343; MUID: 82046808
A: Accession: A61343

A: Molecule type: Protein
A: Residues: 205-298 <BAB>
R: Oeltmeyer, W.; Masson, K.; Kalinna, S.
Eur. J. Biochem. 227, 730-733, 1995
A: Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/
A: Reference number: S69369; MUID: 95172058
A: Accession: S69369

A: Molecule type: Protein
A: Residues: 49-63; 154-168 <OET>
C: Comment: This protein is synthesized in the cytosol and transported into the mitochondr
C: Function:
C: Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A: Note: Located in the inner mitochondrial membrane
C: Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match	Best Local Similarity	Matches	Conservative	Score	DB 1:	Length	DB 2:	Score	DB 3:	Length	DB 4:	Score	DB 5:	Length	DB 6:	Score	DB 7:	Length	DB 8:	Score	DB 9:	Length	DB 10:	Score	DB 11:	Length	DB 12:	Score	DB 13:	Length	DB 14:	Score	DB 15:	Length	DB 16:	Score	DB 17:	Length	DB 18:	Score	DB 19:	Length	DB 20:	Score	DB 21:	Length	DB 22:	Score	DB 23:	Length	DB 24:	Score	DB 25:	Length	DB 26:	Score	DB 27:	Length	DB 28:	Score	DB 29:	Length	DB 30:	Score	DB 31:	Length	DB 32:	Score	DB 33:	Length	DB 34:	Score	DB 35:	Length	DB 36:	Score	DB 37:	Length	DB 38:	Score	DB 39:	Length	DB 40:	Score	DB 41:	Length	DB 42:	Score	DB 43:	Length	DB 44:	Score	DB 45:	Length	DB 46:	Score	DB 47:	Length	DB 48:	Score	DB 49:	Length	DB 50:	Score	DB 51:	Length	DB 52:	Score	DB 53:	Length	DB 54:	Score	DB 55:	Length	DB 56:	Score	DB 57:	Length	DB 58:	Score	DB 59:	Length	DB 60:	Score	DB 61:	Length	DB 62:	Score	DB 63:	Length	DB 64:	Score	DB 65:	Length	DB 66:	Score	DB 67:	Length	DB 68:	Score	DB 69:	Length	DB 70:	Score	DB 71:	Length	DB 72:	Score	DB 73:	Length	DB 74:	Score	DB 75:	Length	DB 76:	Score	DB 77:	Length	DB 78:	Score	DB 79:	Length	DB 80:	Score	DB 81:	Length	DB 82:	Score	DB 83:	Length	DB 84:	Score	DB 85:	Length	DB 86:	Score	DB 87:	Length	DB 88:	Score	DB 89:	Length	DB 90:	Score	DB 91:	Length	DB 92:	Score	DB 93:	Length	DB 94:	Score	DB 95:	Length	DB 96:	Score	DB 97:	Length	DB 98:	Score	DB 99:	Length	DB 100:	Score	DB 101:	Length	DB 102:	Score	DB 103:	Length	DB 104:	Score	DB 105:	Length	DB 106:	Score	DB 107:	Length	DB 108:	Score	DB 109:	Length	DB 110:	Score	DB 111:	Length	DB 112:	Score	DB 113:	Length	DB 114:	Score	DB 115:	Length	DB 116:	Score	DB 117:	Length	DB 118:	Score	DB 119:	Length	DB 120:	Score	DB 121:	Length	DB 122:	Score	DB 123:	Length	DB 124:	Score	DB 125:	Length	DB 126:	Score	DB 127:	Length	DB 128:	Score	DB 129:	Length	DB 130:	Score	DB 131:	Length	DB 132:	Score	DB 133:	Length	DB 134:	Score	DB 135:	Length	DB 136:	Score	DB 137:	Length	DB 138:	Score	DB 139:	Length	DB 140:	Score	DB 141:	Length	DB 142:	Score	DB 143:	Length	DB 144:	Score	DB 145:	Length	DB 146:	Score	DB 147:	Length	DB 148:	Score	DB 149:	Length	DB 150:	Score	DB 151:	Length	DB 152:	Score	DB 153:	Length	DB 154:	Score	DB 155:	Length	DB 156:	Score	DB 157:	Length	DB 158:	Score	DB 159:	Length	DB 160:	Score	DB 161:	Length	DB 162:	Score	DB 163:	Length	DB 164:	Score	DB 165:	Length	DB 166:	Score	DB 167:	Length	DB 168:	Score	DB 169:	Length	DB 170:	Score	DB 171:	Length	DB 172:	Score	DB 173:	Length	DB 174:	Score	DB 175:	Length	DB 176:	Score	DB 177:	Length	DB 178:	Score	DB 179:	Length	DB 180:	Score	DB 181:	Length	DB 182:	Score	DB 183:	Length	DB 184:	Score	DB 185:	Length	DB 186:	Score	DB 187:	Length	DB 188:	Score	DB 189:	Length	DB 190:	Score	DB 191:	Length	DB 192:	Score	DB 193:	Length	DB 194:	Score	DB 195:	Length	DB 196:	Score	DB 197:	Length	DB 198:	Score	DB 199:	Length	DB 200:	Score	DB 201:	Length	DB 202:	Score	DB 203:	Length	DB 204:	Score	DB 205:	Length	DB 206:	Score	DB 207:	Length	DB 208:	Score	DB 209:	Length	DB 210:	Score	DB 211:	Length	DB 212:	Score	DB 213:	Length	DB 214:	Score	DB 215:	Length	DB 216:	Score	DB 217:	Length	DB 218:	Score	DB 219:	Length	DB 220:	Score	DB 221:	Length	DB 222:	Score	DB 223:	Length	DB 224:	Score	DB 225:	Length	DB 226:	Score	DB 227:	Length	DB 228:	Score	DB 229:	Length	DB 230:	Score	DB 231:
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	RESULT	6	
S37210	ADP carrier protein T1 - mouse		
	N:Alternate names: adenine nucleotide carrier		
	C:Species: Mus musculus (house mouse)		
	C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999		
	C:Accession: S37210		
	R:Laplace, C.; Coscet, P.		
	submitted to the EMBL Data Library, September 1993		
	A:Reference number: S37210		
	A:Accession: S37210		
	A>Status: preliminary		
	A:Molecule type: mRNA		
	A:Residues: 1-298 <LA>		
	A:Cross-references: EMBL:X74510; NID:g402627; PIDN:CMA52616.1; PID:g402628		
	C:Genetics:		
	A:Gene: ANCI		
	C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology		
	C:Keywords: duplication; transmembrane protein		
	F:5-99/Domains: ADP,ATP carrier protein repeat homology <ACP1>		
	F:110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>		
	F:207-298/Domains: ADP,ATP carrier protein repeat homology <ACP3>		

Query Match	91.9%	Score 1418;	DB 2;	Length 298;
Best Local Similarity	88.9%;	Pred. No. 8.1e-118;		
Matches 265;	Conservative 19;	Mismatches 14;	Indels	Gaps 0;
OY 1 MTEQAISFAKDFLAGGIAAISKTVAVPIERYKLLLOVQHASKQIADAKYKGIVDCIVR 60	: : : : : : : : : : : : : : : : : : :			
Db 1 MDQDAISFLKEDELAGGIAAAVSKTVAPIERKLLLOVQHASKQIASAKYKGIIIDCVVR 60	: : : : : : : : : : : : : : : : : : :			
OY 61 IPKEGVGISFWMGNLANIYRYRPQALNPAFDKTKOYLFGVDNHKKPFWRFAAGNLASG 120				
Db 61 IPKEGVGSFSEWGNLANIYRFPTQALNPAFDKTKOYLFGVDNHKKPFWRFAAGNLASG 120				
OY 121 GAAGATSLCEFYPLDFAARTRLAADYGKSCTEREFRGLGDCLVKIRKSDGIRGLYGGFSVS 180				
Db 121 GAAGATSLCEFYPLDFAARTRLAADYGKSSORERFNGLGDCLTKIRKSDGLKGLYGGFSVS 180				

OY 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
Db 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 298
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 298

RESULT 7
A44778
ADP, ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP, ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; MUID:89340499
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LTA>
A:Cross-references: GB:J04962; NID:g178658; PIDN:AAA51736.1; PID:g178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A:Reference number: S03893; MUID:89236396
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
A:Reference number: A39891; MUID:88041149
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
R:Experimental source: clone pHMANT
R:Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A:Reference number: A94197; MUID:88124845
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOH>
A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP, ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 5.1e-117;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCVR 60
Db 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCVR 60
OY 61 IPKEGVLSFMRGNLANIYRIFPTQALNFAFKDKKQIFLGVDVNDHTQFMRFAGNLASG 120
Db 61 IPKEGVLSFMRGNLANIYRIFPTQALNFAFKDKKQIFLGVDVNDHTQFMRFAGNLASG 120

Db 61 IPKEGVLSFMRGNLANIYRIFPTQALNFAFKDKKQIFLGVDVNDHTQFMRFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVTKTSKGIGLVGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVTKTSKGIGLVGFSVS 180
OY 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
Db 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 298
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 298

RESULT 8
S31814
ADP, ATP carrier protein T2 - mouse
N:Alternate names: adenine nucleotide translocase
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
R:Costet, P.; Laplace, C.
Submitted to the EMBL Data Library, January 1993
A:Reference number: S31814
A:Accession: S31814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <COS>
A:Cross-references: EMBL:X70847
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;
Best Local Similarity 89.2%; Pred. No. 1.1e-116;
Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCVR 60
Db 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCVR 60
OY 61 IPKEGVLSFMRGNLANIYRIFPTQALNFAFKDKKQIFLGVDVNDHTQFMRFAGNLASG 120
Db 61 IPKEGVLSFMRGNLANIYRIFPTQALNFAFKDKKQIFLGVDVNDHTQFMRFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVTKTSKGIGLVGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGGLDCLVTKTSKGIGLVGFSVS 180
OY 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
Db 181 VGGIIITRAAFVGYDTRAKGMLPDPKNTHTIVSWMIAGTAVAGVSVSPEDTVARRMM 240
OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 296
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNTLRMGCAFVLYLDELKKVI 296

RESULT 9
S31935
ADP, ATP carrier protein - African malaria mosquito
N:Alternate names: Anopheles gambiae (African malaria mosquito)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R:Beard, C.B.; Crews-Owen, A.E.; Collins, F.H.
Submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
A:Reference number: S31935

A:Accession: S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BE>
A:Cross-references: EMBL: Z21814; EMBL: Z21815
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
E:7-101/Domain: ADP, ATP carrier protein repeat homology <ACPI>
E:112-204/Domain: ADP, ATP carrier protein repeat homology <ACF2>
E:209-300/Domain: ADP, ATP carrier protein repeat homology <ACF3>

[illegible]

RESULT 10
T23207
hypothetical protein K01H12.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <WIL>
A:Cross-references: EMBL:Z66218; PIDN:CAA92472.1; GSPDB:GNO00022; CESP:K01H12.2
C:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1: 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

	Query Match	67.5%	Score 1041;	DB 2;	Length 313;
	Best Local Similarity	70.9%;	Pred. No. 1.8e-84;		
	Matches 207;	Conservative 29;	Mismatches 52;	Indels 4;	Gaps
Oy	8 FAKPELGGIAAATSKTAVAPIERVKLLQVHASKQIADKQYGVDCIVRIPIRKEQGV	67			
Dd	25 FLIDIASGTTAAASKTAVAPIERVKLLQVODASTLTITADRRKGIVDVLVRPKEQGY	84			
Oy	68 LSPFNINLANIYIRFPPQALNFAFKDKYKOJELFGVGKHQPMFRYPAGNLASGSAACATS	127			
Dd	85 AALWGNLANIYIRFPQALNFAFKDYKKNIPOKGLPKDKDEMFEPAGNLASGSAACATS	144			
Oy	128 LCFEVPDFARTRLAADVGKSGTEREFPGJGDCLVKITKSDGINGLQGFSVSVOGITIIY	187			

[illegible]

```

RESULT 11
T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25850
R:Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid T01B11.
A:Reference number: Z20099
A:Accession: T25850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-113 <GET>
A:Cross-references: EMBL:U80931; PIDN:AA838001.1; GSPDE:GN00022; CESP:T01B11.4
A:Experimental source: strain Bristol N2; clone T01B11
A:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4
A:Introns: 4/1; 191/2
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

```

	Query Match	67.3%	Score 1039:	DB 2:	Length 313:
	Best Local Similarity	70.9%	Pred. NO. 2.7e-84:		
	Matches	207:	Conservative	29:	Mismatches 52: Indels 4: Gaps 3:
Qy	8	EAKDFLAGGIAAISKTA	TA	TA	TA
		1	1	1	1
		1	1	1	1
Db	25	FLIDLASAGTA	AAVSKTA	TA	TA
		1	1	1	1
		1	1	1	1
Qy	68	LSFMKGNLANV	RYRPTOLANF	APFADKYKQI	ELGVSDH
		1	1	1	1
		1	1	1	1
Db	85	AALHMGNLANV	RYRPTOLANF	APFADKYKQI	ELGVSDH
		1	1	1	1
		1	1	1	1
Qy	128	LCFVYPLDF	PARTRLADY	VGKSGTERE	EPKGLGDCI
		1	1	1	1
		1	1	1	1
Db	145	LCFVYPLDF	PARTRLADY	VGKSGTERE	EPKGLGDCI
		1	1	1	1
		1	1	1	1
Qy	188	RAAYFGVDTA	KGMLPPDRK	NTHIVASNM	ITATVA
		1	1	1	1
		1	1	1	1
Db	204	RAAYFGVDTA	KGMLPPDRK	NTHIVASNM	ITATVA
		1	1	1	1
		1	1	1	1
Qy	247	ADIMTGYVDC	RRKTFRDE	GKAFKRG	ASNVLR
		1	1	1	1
		1	1	1	1
Db	263	DVLTAKNPLD	CAVKTIIK	NEGASAMK	AGALSIN
		1	1	1	1
		1	1	1	1

RESULT 12
T25371
hypothetical protein T27E9.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20024
A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <MIL>
A:Cross-references: EMBL:Z82059; PIDB:CAE04874.1; GSPDB:GN00021; CESP:T27E9.1

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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:33:12 ; Search time 57.26 Seconds

(without alignments)
385.502 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGIAAA.....LRGKGAFVLYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq-1101:*

- 1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID58/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID58/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID58/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID58/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID58/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID58/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1543	100.0	298	21	AAV71033	Human adenine nucl
2	1543	100.0	298	22	AAV39641	Human polypeptide
3	1543	100.0	298	22	AAU01200	Human adenine nucl
4	1543	100.0	298	22	AAV41427	Human polypeptide
5	1454	94.2	298	21	AAV71032	Human adenine nucl
6	1454	94.2	298	22	AAU01199	Human adenine nucl
7	1412	91.5	298	19	AAV61169	Anli protein. Mus
8	1385.5	89.8	297	21	AAV71031	Human adenine nucl
9	1385.5	89.8	297	22	AAU01198	Human adenine nucl
10	749.5	48.6	386	22	AAU00106	ADP/ATP carrier pr
11	742.5	48.1	346	21	AAV36577	Arabidopsis thalia

12	742.5	48.1	346	21	AAV37261	Arabidopsis thalia
13	742.5	48.1	346	21	AAV37264	Arabidopsis thalia
14	742.5	48.1	346	21	AAV38460	Arabidopsis thalia
15	742.5	48.1	363	21	AAV36576	Arabidopsis thalia
16	742.5	48.1	363	21	AAV37260	Arabidopsis thalia
17	742.5	48.1	363	21	AAV37263	Arabidopsis thalia
18	742.5	48.1	363	21	AAV38459	Arabidopsis thalia
19	742.5	48.1	381	21	AAV36575	Arabidopsis thalia
20	742.5	48.1	381	21	AAV37259	Arabidopsis thalia
21	742.5	48.1	381	21	AAV37262	Arabidopsis thalia
22	742.5	48.1	381	21	AAV38458	Arabidopsis thalia
23	742.5	48.1	992	21	AAV38672	Arabidopsis thalia
24	742.5	48.1	1009	21	AAV38671	Arabidopsis thalia
25	742.5	48.1	1027	21	AAV38670	Arabidopsis thalia
26	739.5	47.9	346	21	AAV17731	Arabidopsis thalia
27	739.5	47.9	363	21	AAV17730	Arabidopsis thalia
28	739.5	47.9	381	21	AAV17729	Arabidopsis thalia
29	689.5	44.7	330	21	AAV20658	Arabidopsis thalia
30	688.5	44.6	330	21	AAV39398	Arabidopsis thalia
31	679.5	44.0	333	21	AAV06857	Arabidopsis thalia
32	679.5	44.0	333	21	AAV06856	Arabidopsis thalia
33	679.5	44.0	368	21	AAV06855	Arabidopsis thalia
34	672	43.6	306	21	AAV12916	Arabidopsis thalia
35	672	43.6	306	21	AAV16974	Arabidopsis thalia
36	659.5	42.7	291	21	AAV20659	Arabidopsis thalia
37	658.5	42.7	291	21	AAV39399	Arabidopsis thalia
38	654	42.4	291	21	AAV12917	Arabidopsis thalia
39	654	42.4	291	21	AAV16975	Arabidopsis thalia
40	588.5	38.1	263	21	AAV12918	Arabidopsis thalia
41	588.5	37.9	249	21	AAV16976	Arabidopsis thalia
42	585.5	37.9	249	21	AAV20660	Arabidopsis thalia
43	584.5	37.1	249	21	AAV39400	Arabidopsis thalia
44	572.5	37.1	312	21	AAV28188	Arabidopsis thalia
45	563.5	36.5	228	21	AAV28189	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV71033	standard; Protein; 298 AA.
XX	XX
AC	AAV71033;
XX	XX
DT	29-AUG-2000 (first entry)
XX	XX
DE	Human adenine nucleotide translocator ANT3.
XX	XX
XX	Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neurotropic;
KW	antiparkinson; cerebroprotective; therapeutic; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDP;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
OS	Homo sapiens.
XX	XX
PN	WO200026370-A2.
XX	XX
PD	11-MAY-2000.
XX	XX
PF	03-NOV-1999; 99WO-US25883.
XX	XX
PR	03-NOV-1998; 98US-0185904.
XX	XX
PA	08-SEP-1999; 99US-0393441.
XX	XX
XX	(MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX WPI: 2000-365619/31.
DR N-PSDB: AAD00521.
XX
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX
PS Claim 46; Page 173-174; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 21; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASQIADKQYGIYDCIVR 60
DB 1 mteqaisfakdfliaggiaaistavapiervklllqvhaaskqiaadkqygiydcivr 60
QY 61 IRKEGVLSFMRGNLANVRYRFPQTQALNFAFKDKYKQIFLGVDKHTQWRPFAGNLSG 120
DB 61 ipkegvlsfmrgnlanvryrftqalnfafdkyqkqiflgvdktqwrpfagnlsag 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFRGLDCLVKIRKSDGIRLYOGFSVS 180
DB 121 gaagatslcfvypldfartrlaadvgksgterefrgldclvki rksdgi rlyogfsvs 180
QY 121 gaagatslcfvypldfartrlaadvgksgterefrgldclvki rksdgi rlyogfsvs 180
DB 121 gaagatslcfvypldfartrlaadvgksgterefrgldclvki rksdgi rlyogfsvs 180
QY 181 VGGIIIRAAVYGVYDTAKGMLPDKNTHIVVSWMAIQVTVAAGVSYPFDTVRRMM 240
DB 181 vggiiiraaavygyvdtakgmlpdknthi vswmaiaqvtaavgsy pfdtvt rrrmm 240
QY 241 OSGRKGADIMYGTWCWKRIFRDEGKAFPGAMSNVLRGGAFAVLVYDELKKVI 298
DB 241 osgrkgadimygwtcwkrifrd egkafpgamsnv lrggaafavlvydelkkvi 298

RESULT 2
AAM39641
ID AAM39641 standard; Protein: 298 AA.
XX
XX AAM39641;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2786.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW Leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX
XX 26-JUL-2001.
XX
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Dimaac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB: AA158797.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localized neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC assays for receptor activity, arthritis and inflammation, leukaemias and CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed CC specification.

Query Match 100.0%; Score 1543; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASQIADKQYGIYDCIVR 60
DB 1 mteqaisfakdfliaggiaaistavapiervklllqvhaaskqiaadkqygiydcivr 60
QY 61 IRKEGVLSFMRGNLANVRYRFPQTQALNFAFKDKYKQIFLGVDKHTQWRPFAGNLSG 120
DB 61 ipkegvlsfmrgnlanvryrftqalnfafdkyqkqiflgvdktqwrpfagnlsag 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFRGLDCLVKIRKSDGIRLYOGFSVS 180
DB 121 gaagatslcfvypldfartrlaadvgksgterefrgldclvki rksdgi rlyogfsvs 180
QY 181 VGGIIIRAAVYGVYDTAKGMLPDKNTHIVVSWMAIQVTVAAGVSYPFDTVRRMM 240
DB 181 vggiiiraaavygyvdtakgmlpdknthi vswmaiaqvtaavgsy pfdtvt rrrmm 240

QY 241 QSGRKAGDIWYTGTVDCWKRKIFRDEGKAFKFGKAMSNVLRMGAGFVLYLYDELKKVI 298
 |||
 DB 241 qsgrrkgadlmvgtvdcwrkifrdggkafkfgkawsnvrlgmgaafvlylydelkkvi 298

RESULT 3

AAU01200

ID AAU01200 standard; Protein; 298 AA.

AC AAU01200;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-3 (ANT-3) protein.

KW Human; adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN MO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US30535.

PR 03-NOV-1999; 99US-0434354.

PA (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frliger LG;

PI Vellosceli G, Davis RE;

DR WPI: 2001-291054/30.

DR N-PSDB: AAS05903.

PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 IT fused to energy transfer molecule -

PS Disclosure; Fig 2; 186pp; English.

CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SO Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 22; Length 298;

Best Local Similarity 100.0%; Pred. No. 2,5e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDIAGIAAISTKTAVERKLLLOVGHASKOIADKOYKGIYDCTVR 60

DB |||
 1 mtegaistsfakdfiaaglaaistktaavlervklllvqbnaskqiaadkqyglvdcivr 60
 QY 61 IPKEGCVLSFWRGNLANVIRFPTQALNFAFKDKYKOIFLGVDKHTQFRRFRAGNLASG 120
 |||
 DB 61 ipkegcvlsfwrnlanvlyrfptqalnfafkdkykgiflgvdkhqtqfrrfragnlasg 120
 QY 121 GAAGATSLCFVYPLDFARTPLADVCGSKREPERGSGDCLVITKTSDSGIRGLYOGFSVS 180
 |||
 DB 121 gaagatslcfvypldfartpladvgksrereprgsgdclvltktsdglrlyqgfsvs 180
 QY 181 VGGIITVRAAYFGVYDTAKGMLDPKNTHTIVSGMIAQVTAAGVVSYPFDVRRRMM 240
 |||
 DB 181 vggilyraayfgvydtakgmlpdknthivsgmialqvtaagvvsypfdvrrrrmm 240
 QY 241 QSGRKAGDIWYTGTVDCWKRKIFRDEGKAFKFGKAMSNVLRMGAGFVLYLYDELKKVI 298
 |||
 DB 241 qsgrrkgadlmvgtvdcwrkifrdggkafkfgkawsnvrlgmgaafvlylydelkkvi 298

RESULT 4

AAM41427

ID AAM41427 standard; Protein; 323 AA.

AC AAM41427;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6358.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukemia.

OS Homo sapiens.

PN MO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US34263.

PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI: 2001-442253/47.

DR N-PSDB: AA160583.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

PS Example 2; SEQ ID NO 6358; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 323 AA:

Query Match 100.0%; Score 1543; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASKQIADKQYGVDCIYR 60
 DB |||||||
 DB 26 mteqaisfakdfliaggaiaaistavapiervklllqvghaskqlaadkqygvdciv 85
 QY 61 IREEGVLSFMGKGLANVRYRFPQTALNFAFKDKYKQIFLGVDKHTQFWRFAAGNLASG 120
 DB |||||||
 DB 86 IREEGVLSFMGKGLANVRYRFPQTALNFAFKDKYKQIFLGVDKHTQFWRFAAGNLASG 145
 QY 121 GAAGATSLCFVYPLDFARLADYVKSSTEREFGIGDCLVTKIRKSDIRLQYGFYSV 180
 DB |||||||
 DB 146 gaagatslcfvypldfarladyvkssterefgigdcivtkirsdgtrlyqgfysv 205
 QY 181 VOGIITRYRAAYGVYDTAKGMLPDKNTHIVVSMIAQTVAAGVSYPEPTVRRRMM 240
 DB |||||||
 DB 206 vogiitryraaygvdydtakgmldpdknthiivvsmiaqvtavagvsypfdtvrmmmm 265
 QY 241 GSGRGADIMYGTGDCWKIRFDEGSKAFKFGAMSNVIRGSGAFVILVYDELKKVI 298
 DB |||||||
 DB 266 gsgrgadimygtdcwkirfdegskafkfgamsnvlrsgsagfavlvydelkkvi 323

RESULT 5
 AAY71032
 ID AAY71032 standard; Protein; 298 AA.

XX AAY71032;

XX 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANT2.

XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotrophic;
 KW antiparkinsonian; cytoprotective; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

XX WO2000026370-A2.

XX 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

XX 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX WPI: 2000-365619/31.

DR N-PSDB: AAD00520.

PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease

PS Claim 45; Page 172-173; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.

XX Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 21; Length 298;
 Best Local Similarity 92.6%; Pred. No. 8.9e-148;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASKQIADKQYGVDCIYR 60
 DB ||:|||||
 DB 1 mteqaisfakdfliaggaiaaistavapiervklllqvghaskqlaadkqygvdciv 60
 QY 61 IREEGVLSFMGKGLANVRYRFPQTALNFAFKDKYKQIFLGVDKHTQFWRFAAGNLASG 120
 DB |||||||
 DB 61 IREEGVLSFMGKGLANVRYRFPQTALNFAFKDKYKQIFLGVDKHTQFWRFAAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARLADYVKSSTEREFGIGDCLVTKIRKSDIRLQYGFYSV 180
 DB |||||||
 DB 121 gaagatslcfvypldfarladyvkssterefgigdcivtkirsdgtrlyqgfysv 180
 QY 181 VOGIITRYRAAYGVYDTAKGMLPDKNTHIVVSMIAQTVAAGVSYPEPTVRRRMM 240
 DB |||||||
 DB 181 vogiitryraaygvdydtakgmldpdknthiivvsmiaqvtavagvsypfdtvrmmmm 240
 QY 241 GSGRGADIMYGTGDCWKIRFDEGSKAFKFGAMSNVIRGSGAFVILVYDELKKVI 296
 DB |||||||
 DB 241 gsgrgadimygtdcwkirfdegskafkfgamsnvlrsgsagfavlvydelkkvi 296

RESULT 6

AAU01199
 ID AAU01199 standard; Protein; 298 AA.

XX AAU01199;

XX 07-SEP-2001 (first entry)

XX Human adenine nucleotide translocator-2 (ANT-2) protein.

XX Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX	Homo sapiens.
OS	
XX	
PN	MO200132876-A2.
XX	
PD	10-MAY-2001.
XX	
PF	03-NOV-2000; 2000MO-US30535.
XX	
PR	03-NOV-1999; 99US-0434354.
XX	
PA	(MITO-) MITOKOR.
XX	
PI	Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI	Vellicelebi G, Davis RE;
XX	
DR	MP1: 2001-291054/30.
DR	N-PSDB: AAS05902.
XX	
PT	New nucleic acid expression constructs, useful for screening for agents
PT	that alter mitochondrial permeability transition (MPT), comprises
PT	polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT	used to energy transfer molecule -
XX	
SS	Disclosure: Fig 2; 186pp; English.

```

Db      121 gaagatslfvypldarftrlaadvkgsqrefngldclikfkfsgdklqlygfsvs 180
OY      181 VGGIITRYRAAYGVYDTAKGMLPDPKNTIHVSWMIAGTVAAGVSYFPDTRRRMM 240
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 vggillyraaygyvdtakgmlpdpknvhlfswmiaqsvtaagllsyfddvrrrrmm 240
OY      241 GSGRKADIMYGTVDCKWRKIFRDEGKAFFKGAMSNVLRGKGAFVLYLYDELKVI 298
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 gsgrkadimygtdcwrkfrdegakafkfgawsnvlrimgafvlylydelkkyv 298

RESULT 8
AA071031
ID      AA071031 standard; Protein: 297 AA.
AC      AA071031;
DE      29-AUG-2000 (first entry)
XX      Human adenine nucleotide translocator ANT1.
XX      Human: adenine nucleotide translocator: ANT1; mitochondria; ADP; ATP;
XX      adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX      mitochondrial permeability transition; neuroprotective; neurotrophic;
XX      antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
XX      antidepressant; cerebroprotective; therapeutic; screening; psoriasis;
XX      Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX      diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX      mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
XX      mitochondrial diabetes and deafness; hyperproliferative disorder;
XX      myoclonic epilepsy red ragged fibre syndrome.
XX      Homo sapiens.
XX      WO200026370-A2.
XX      11-MAY-2000.
XX      03-NOV-1999; 99WO-US25883.
XX      03-NOV-1998; 98US-0185904.
XX      08-SEP-1999; 99US-0393441.
XX      (MITO-) MITOKOR.
XX      Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
XX      Ghosh SS;
XX      WPI: 2000-365619/31.
XX      N-PSDB: AAD00519.
XX      Recombinant construct encoding adenine nucleotide translocator
XX      polypeptide, useful e.g. in screening for potential therapeutic agents
XX      against mitochondrial disease -
XX      Claim 44; Page 172; 175pp; English.
XX      The patent discloses a method to produce adenine nucleotide translocator
XX      (ANT) proteins or ANT fusion proteins using recombinant expression
XX      constructs. ANT is a nuclear encoded protein and a major component of
XX      inner mitochondrial membrane. It mediates transport of adenosine
XX      di/tri-phosphates across the mitochondrial inner membrane and also serves
XX      as an important molecular component of the mitochondrial permeability
XX      transition pore, a modulator of apoptosis. ANT is used to identify agents
XX      or ligands that bind to, or interact with it. The ANT ligands are used to
XX      detect or isolate ANT in a biological sample, and therapeutically for
XX      regulating mitochondrial pore activity, for treating diseases associated
XX      with altered mitochondrial function, including Alzheimer's, Parkinson's
XX      and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX      Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX      encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX      disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
XX      epilepsy red ragged fibre syndrome. The present sequence is an

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CC      adenine nucleotide translocator ANT1 from human brain.
XX      SQ
XX      Sequence      297 AA:
Query Match      89.8%; Score 1385.5; DB 21; Length 297;
Best Local Similarity 87.2%; Pred. No. 2e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
OY      1 MTEOATSPAKDFLAGIAAISKTAAPERVKLLLOVHASKOIAADKQYGIYDCIAR 60
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Db      1 mgdhawsfikdflagavaaavsktavapiervklllyqvnaskqysaekyqgllidcvrr 60
OY      61 IPEQGVLSFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGVGVDRHTQFMRFAAGNLASG 120
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Db      61 ipkeggfslsfrgnlanviryfrtqalnfaefdkykqiflfgvdrhtkqfwryfaaglnasg 120
OY      121 GAAGATSLCFYVPDPFARRLAADYKSGSTEREKFGICGLYKTRKSDGIRLQYGFVS 180
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OY      181 VGGIITRYRAAYGVYDTAKGMLPDPKNTIHVSWMIAGTVAAGVSYFPDTRRRMM 240
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Db      180 vggillyraaygyvdtakgmlpdpknvhlfswmiaqsvtaagllsyfddvrrrrmm 239
OY      241 GSGRKADIMYGTVDCKWRKIFRDEGKAFFKGAMSNVLRGKGAFVLYLYDELKVI 298
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RESULT 9
AA001198
ID      AA001198 standard; Protein: 297 AA.
AC      AA001198;
DE      07-SEP-2001 (first entry)
XX      Human adenine nucleotide translocator-1 (ANT-1) protein.
XX      Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
XX      mitochondrial permeability transition pore component; cell survival;
XX      mitochondrial core component; mitochondrial related disorder; cancer;
XX      Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX      Homo sapiens.
XX      WO200132876-A2.
XX      10-MAY-2001.
XX      03-NOV-2000; 2000WO-US30535.
XX      03-NOV-1999; 99US-0434354.
XX      (MITO-) MITOKOR.
XX      Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
XX      Velicelebi G, Davis RE;
XX      WPI: 2001-291054/30.
XX      N-PSDB: AAS05901.
XX      New nucleic acid expression constructs, useful for screening for agents
XX      that alter mitochondrial permeability transition (MPT), comprises
XX      polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
XX      fused to energy transfer molecule -
XX      Disclosure: Fig 2; 186pp; English.
XX      The present sequence represents human adenine nucleotide translocator-1
XX      (ANT-1) protein. ANT proteins are mitochondrial permeability
XX      transition (MPT) pore components responsible for mediating transport

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SQ Sequence 297 AA;

1

4

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 9905-011825.
PR 05-MAR-1999; 9905-0123180.
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QY 64 EGVVLSFWRGNLNVIRYFTQALNFAFKKYYQIFLGVDKHTQFWRYFAGNLASGAA 123
DB 102 deGfsglwtgrntanvlyfptqalnfaFkdyfKrlInfkKdr-dgykwkwlagnlaSgaa 160
QY 124 GATSLCFVYVLDPAFRTPLAD---VCKSGTEREFRCIGDCLVKTITKSDGIRGLYOGCSVS 180
DB 161 gassllfvyldvartclandakaakkggsgqfddglvdvrytklktkdglaglyrgfnls 220
QY 181 VGIIIRYRAAYFCGVYDTAK-----GMLPDPKNTIIVVSMIAQTVTAAGVSTYPTVR 235
DB 221 cvglfvyrglyfglydsvkvklltgdldqdsffasfalgwI---tnagaglasypIdtvr 276
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
PN EPI033405-r2.
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PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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XX AAG37264;
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XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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XX Arabidopsis thaliana.
OS
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DT	18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44844.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

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PN EP1033405-A2.

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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.

PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160747.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.1%; Score 742.5; DB 21; Length 363;
Best Local Similarity 52.8%; Pred. No. 2,8e-71;
Matches 160; Conservative 45; Mismatches 77; Indels 21; Gaps 7;

OY 7 SFAKDFLAGGIAAIAISKTAVAPIERVKLLQVOHASQOIA---DKOYKGIYDCIYRIPK 63
DB 61 nfaIdflmgysaaavaktaapierkvlllqng--demlaagrlsepykldgcfrtlk 118
OY 64 EOGVLSFMRGNLANVIRYFPTQALNFAFKDKYQOIFLGVDKHTQOFMRYPAGNLASGAA 123
DB 119 degfsglwrntanvlrlyftqelnfafkdyfkrllfnfkdr-dgywkwfagnlaasgae 177
OY 124 GATSLCFVYPLDARFRLAD---VGKSTREPERRGDCLVYITKSDGRGLYQGSVS 180
DB 178 gassllfvysldyartlrlandakaakxg99rfgdldvdyrtklkdglaglyrgfnls 237
OY 181 VOGIIIRAAVFCVYDTAK-----GMLPDPKNTIHVSMIAOTVPAAGVSVYPTVR 235
DB 238 cvglilvyrglyfgyldsvkvvlltgdldqdsffasfalgwvl-----tngeglasypldtr 293
OY 236 RRMWOSGRKGDIMYTGIVDCWRKRIFRDEGKAFFKGANSNVLRGNGAFVLVIDELK 295
DB 294 rmmmtsgea---vkxssidafkqllknegakslfkagaganllravagagvlsydklg 350
OY 296 KVI 298
DB 351 IIV 353

Search completed: February 13, 2002, 09:33:13
Job time: 110 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 : Search time 55.37 Seconds
(without alignments)
784.592 Million cell updates/sec

Title: US-09-393-441-31
Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGVA...LRGMAFLVLVDKIKYV 297

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP Vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464.5	94.3	298	6	046373 Oryctolagus
2	1463.5	94.2	298	1	062164 mus musculu
3	1377.5	88.7	298	13	09YIC4 Oryctolagus
4	1377.5	88.7	298	13	09PRH1 Oryctolagus
5	1374.5	88.5	298	13	09PRH2 Oryctolagus
6	1366.5	88.0	298	13	0919M9 Oryctolagus
7	1241.5	79.9	300	5	09NHWS Oryctolagus
8	1234.5	79.5	317	13	091336 Oryctolagus
9	1183	76.2	288	5	044093 Oryctolagus
10	1183	76.2	288	5	044094 Oryctolagus
11	1147	73.9	307	5	062526 Oryctolagus
12	1139.5	73.4	304	5	025129 Oryctolagus
13	1101.5	70.9	315	4	09HOC2 Oryctolagus
14	1045.5	67.3	313	5	091410 Oryctolagus
15	1043.5	67.2	313	5	021103 Oryctolagus
16	1037.5	66.8	300	5	045865 Oryctolagus
17	1003.5	64.7	300	5	001813 Oryctolagus
18	993.5	64.0	300	5	017407 Oryctolagus
19	989.5	63.7	309	5	097470 Oryctolagus

20	959	61.8	307	8	09XM22 Oryctolagus
21	950	61.2	318	5	09B136 Oryctolagus
22	905.5	58.3	301	5	025692 Oryctolagus
23	904.5	58.2	301	5	026006 Oryctolagus
24	841.5	54.2	170	6	09XS69 Oryctolagus
25	772	49.7	306	5	018683 Oryctolagus
26	757.5	48.8	305	3	09P8M1 Oryctolagus
27	750.5	48.3	307	5	076286 Oryctolagus
28	748.5	48.2	303	3	074260 Oryctolagus
29	746.5	48.0	379	10	049447 Oryctolagus
30	745.5	48.0	326	5	091270 Oryctolagus
31	743.5	47.9	307	5	026697 Oryctolagus
32	740.5	47.7	386	10	093767 Oryctolagus
33	738.5	47.6	388	10	049875 Oryctolagus
34	731.5	47.1	317	5	09N647 Oryctolagus
35	731	47.1	385	10	09P152 Oryctolagus
36	728.5	46.9	306	3	078754 Oryctolagus
37	727.5	46.8	331	10	041628 Oryctolagus
38	708	45.6	305	3	09P876 Oryctolagus
39	705	45.4	305	3	09P875 Oryctolagus
40	681	43.9	330	10	09PM86 Oryctolagus
41	676	43.5	298	5	021809 Oryctolagus
42	659	42.4	262	10	09AVT6 Oryctolagus
43	508	32.7	327	10	09LF44 Oryctolagus
44	486	31.3	162	5	026130 Oryctolagus
45	461	29.7	158	5	076467 Oryctolagus

ALIGNMENTS

RESULT 1
ID 046373 PRELIMINARY; PRT; 298 AA.
AC 046373;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELTAL MUSCLE;
RA Yamaguchi N., Kasai M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BAA23777.1; -
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; Mitoc_carf; 3.
DR PRINTS; PS00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAFA32C8B164AD78 CMC64;

Query Match 94.3%; Score 1464.5; DB 6; Length 298;
Best Local Similarity 94.6%; Pred. No. 1.2e-126;
Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVA...KTA...P...R...K...L...V...O...H...S...K...O...I...S...A...K...O...Y...K...G...I...D...C...Y...V...R... 60
DB 1 MSDFHMSFLKDFLAGVA...KTA...P...R...K...L...V...O...H...S...K...O...I...S...A...K...O...Y...K...G...I...D...C...Y...V...R... 60
OY 61 IREKGFSLFNGNLANVIRYPTQALNFAFKDKYKFLGVDNKHKQFWRFFAGNLASG 120
DB 61 IREKGFSLFNGNLANVIRYPTQALNFAFKDKYKFLGVDNKHKQFWRFFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 180
 QY 180 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 239
 DB 181 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 240
 QY 240 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 297
 DB 241 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 298

RESULT 2
 ID 062164 PRELIMINARY; PRT; 298 AA.
 AC 062164;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE TRANSLOCATOR). MEMBER 4).
 DE TRANSLOCATOR). MEMBER 4).
 GN SLC25A4 OR MAMC1 OR ANTI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 QX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=MUSCLE;
 RA Laplace C.; Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF240002; CA52616.1; -;
 DR EMBL: AF240002; AAF64470.1; -;
 DR EMBL: BC003791; AA03791.1; -;
 DR MGD: MGI:1353495; SLC25A4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mlt_carrier.3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER.3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport. SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 94.2%; Score 1463.5; DB 11; Length 298;
 Best Local Similarity 94.0%; Pred. No. 1.5e-126;
 Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVGHASKQISAERKQYGIIDCV 60
 DB 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVGHASKQISAERKQYGIIDCV 60
 QY 61 IPKQGLSLFWRGKLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
 DB 61 IPKQGLSLFWRGKLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 180

DB 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 180
 QY 180 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 239
 DB 181 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 240
 QY 240 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 297
 DB 241 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 298

RESULT 3
 ID 09YIC4 PRELIMINARY; PRT; 298 AA.
 AC 09YIC4;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DE ADP/ATP TRANSLOCASE.
 DE ADP/ATP TRANSLOCASE.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 QX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:99083429; PubMed:9866197;
 RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes of a sex-linked gene, ADP/ATP translocase."
 RT Z. W. X. and Y. in the frog Rana rugosa, inferred from the sequences of mol. Biol. Evol. 15:1612-1619(1998).
 RL -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BA85607.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mlt_carrier.3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER.3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport. SEQUENCE 298 AA; 33068 MW; 15B270BD3709A00 CRC64;

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1.2e-118;
 Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVGHASKQISAERKQYGIIDCV 60
 DB 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVGHASKQISAERKQYGIIDCV 60
 QY 61 IPKQGLSLFWRGKLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
 DB 61 IPKQGLSLFWRGKLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGR-RAQREFHGLGDCIIRKSDGLKLYOGFNV 180
 QY 180 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 239
 DB 181 VGGIITIRAAVFGYVDTAKGMLPDPKNVHIFVSMIAQSTVAAGLVSYPFDVRRMM 240
 QY 240 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 297
 DB 241 QSGRKADIMYGTGDCWKRIADDEGAKAFKGAWSNVLRGMAFVLYLDEIKKYV 298

RESULT 4
 09PRH1

DR EMBL: AF231347; AAE63471.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Transmembrane; Transport.
 DR SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 88.0%; Score 1366.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 1.2e-117;
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 DB 1 MTDAAISFKADFLAGVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 OY 61 IPKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 179
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 180
 OY 180 VGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTVAGLSYFPTVRRRM 239
 DB 180 VGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTVAGLSYFPTVRRRM 239
 OY 240 OSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 297
 DB 240 OSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 297
 OY 241 OSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 298
 DB 241 OSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 298

RESULT 7
 OGNHMS PRELIMINARY: PRT; 300 AA.
 AC OGNHMS;
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ADP/ATP TRANSLUCASE.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestridae; Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Fair J.A., Batterham P.;
 RL "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 RL Submitted (Dec-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: AF218587; AAF32322.1; -.
 CC InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Transmembrane; Transport.
 DR SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
 Best Local Similarity 78.7%; Pred. No. 3.9e-106;
 Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 57
 DB 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 57
 OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 60
 DB 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 60
 OY 58 VRIKKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 117
 DB 58 VRIKKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 117
 OY 61 FVIRKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 120
 DB 61 FVIRKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 120
 OY 118 ASGAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 177
 DB 121 ASGAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 180
 OY 178 VSVGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTVAGLSYFPTVRRRM 237
 DB 181 VSVGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTVAGLSYFPTVRRRM 240
 OY 238 NMOSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 297
 DB 241 NMOSGRKGADIMYTGTVDCWKRKIADEGAKAFKFGANSVLRGNGAFVLYLDEIKRYV 300

RESULT 8
 OGNHMS PRELIMINARY: PRT; 317 AA.
 AC OGNHMS;
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ADP/ATP TRANSLUCASE.
 OS Rana sylvatica (wood frog).
 OC Eukaryota; Metazoa; Chordata; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 RT in wood frogs under freezing stress.";
 RL Biochim. Biophys. Acta 1353:69-76(1997).
 RN [2]
 RP REVISIONS.
 RA Cai Q., Storey K.B.;
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: U44832; AAA97882.2; -.
 CC InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Repeat; Transmembrane; Transport.
 DR SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 1.9e-105;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 60
 DB 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCV 60
 OY 61 IPKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEGGFLSFWNGNLNANVIRFPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLDCIIRKSDGLRGLYOGFNV 180


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OY 180 VGGIIYRAAFGVDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 239
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VGGIIYRAAFGVDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 240

OY 240 OSGRKADIMYGTVDKWRKIAKDEGAKAFK 271
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 OSGRKAEIIMSGTIDCKMKIARDEGGAFFR 272

RESULT 9
ID 044093 PRELIMINARY: PRT: 288 AA.
AC 044093:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE (FRAGMENT).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025798; AAB87883.1; -.
DR Flybase: FBgn0023292; Dpse\sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
FT SEQUENCE 288 AA; 31725 MW; 052B0CC050436B0 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 8, 9e-101;
Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

OY 5 AMSFLKDLAAGAAVAAVSTAVAPIERVKLLQVHASKOISAEKOYKGIIDCVRIKPE 64
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 AIGFVDFAGAGISAAVSTAVAPIERVKLLQVHASKOISAEKOYKGIIDCVRIKPE 66

OY 65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHOFWRFFAGNLSAGGAG 124
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 OGSSSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHOFWRFFAGNLSAGGAG 126

OY 125 ATSLCFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSGDLGKLYOGFVNSVOGII 184
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 ATSLCFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSGDLGKLYOGFVNSVOGII 186

OY 185 IYRAAFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMMOSGRK 244
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 IYRAAFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMMOSGRK 245

OY 245 GADIMYGTVDKWRKIAKDEGAKAFKGAFAFVNLRGMGAFVLY 288
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 246 ATEIIYKNTLHCWGTIAKDEGSAFFKGAFAFVNLRGMGAFVLY 288

RESULT 10
ID 044094 PRELIMINARY: PRT: 288 AA.
AC 044094:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
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DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE (FRAGMENT).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025799; AAB87884.1; -.
DR Flybase: FBgn0023237; Dsub\sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
FT SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 8, 9e-101;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

OY 5 AMSFLKDLAAGAAVAAVSTAVAPIERVKLLQVHASKOISAEKOYKGIIDCVRIKPE 64
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 7 AMGFVDFAGAGISAAVSTAVAPIERVKLLQVHASKOISAEKOYKGIIDCVRIKPE 66

OY 65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHOFWRFFAGNLSAGGAG 124
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 67 OGSSSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHOFWRFFAGNLSAGGAG 126

OY 125 ATSLCFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSGDLGKLYOGFVNSVOGII 184
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 127 ATSLCFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSGDLGKLYOGFVNSVOGII 186

OY 185 IYRAAFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMMOSGRK 244
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 187 IYRAAFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLLSYPTDVRRRMMOSGRK 245

OY 245 GADIMYGTVDKWRKIAKDEGAKAFKGAFAFVNLRGMGAFVLY 288
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 246 ATEIIYKNTLHCWGTIAKDEGSAFFKGAFAFVNLRGMGAFVLY 288

RESULT 11
ID 062526 PRELIMINARY: PRT: 307 AA.
AC 062526:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANT2 PROTEIN.
GN ANT2 OR CG1683.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BERKELEY.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandlides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunlov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kenlson J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrstkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.C., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RA Zhang Y.Q., Davis A.W., Rote J., Ashburner M.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003484; AAF47956.1; -;
 DR EMBL: Y10618; CAA71629.1; -;
 DR FlyBase; FBgn0025111; Ant2.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN 2.
 SQ SEQUENCE 307 AA; 33744 MW; 306B3DFD82061C0C CRC64;

Query Match 73.9%; Score 1147; DB 5; Length 307;
 Best Local Similarity 73.8%; Pred. No. 2e-97;
 Matches 214; Conservative 33; Mismatches 43; Indels 0; Gaps 0;

QY 7 SPLKFLGAAVAANSKRAVPIERVKLLQVQASHAKOISAEKQKGIIDCVVRIPKEOG 66
 DB 17 SFLDMFMGVSAAIAKTAAPIERVKLLQVQASHAKOISAEKQKGIIDCVVRIPKEOG 76
 QY 67 FLSEFRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDRHKOFWYFNGNLANSGAAGT 126
 DB 77 FSSFRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDRHKOFWYFNGNLANSGAAGT 136
 QY 127 SLCEFYPLDFAFTRIAADVGRRAROREFHGLGDCIIRKFSKDSGLRGLXOGFNVSVOGIITY 186
 DB 137 SLCEFYPLDFAFTRIAADVGRRAROREFHGLGDCIIRKFSKDSGLRGLXOGFNVSVOGIITY 196
 QY 187 RAAFGVYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSGRGA 246
 DB 197 RAAFGVYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSGRGA 256
 QY 247 DIMYGTGDCNRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKY 296

DB 257 EMYNKATAHCMVLVIAKOGIGAFKFGALSNITRGALVLYLDEMKKY 306
 RESULT 12
 ID 025129 PRELIMINARY; PRT; 304 AA.
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ADP/ATP TRANSLOCASE.
 GN HRAVL.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyrosidae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Miya T., Makebe K., Satoh N.;
 RT "Expression of a gene for major mitochondrial protein, ADP/ATP
 RT translocase, during embryogenesis in the ascidian *Halocynthia*
 RT roretzi.";
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY)
 CC -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: D83069; BA01765.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 304 AA; 33306 MW; 51FD0D7D6B654880 CRC64;

Query Match 73.4%; Score 1139.5; DB 5; Length 304;
 Best Local Similarity 74.6%; Pred. No. 9.6e-97;
 Matches 220; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

QY 6 WS--FLKDFLAGAAVAANSKRAVPIERVKLLQVQASHAKOISAEKQKGIIDCVVRIP 62
 DB 3 WSAVDFAKDLAIGTAAAIKTIYPIERVKLLQVQASHAKOISAEKQKGIIDCVVRIP 62
 QY 63 KEQGFSLMRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDRHKOFWYFNGNLANSGA 122
 DB 63 KEQGFSLMRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDRHKOFWYFNGNLANSGA 122
 QY 123 AGATSLCEFYPLDFAFTRIAADVGRRAROREFHGLGDCIIRKFSKDSGLRGLXOGFNVSVOG 182
 DB 123 AGATSLCEFYPLDFAFTRIAADVGRRAROREFHGLGDCIIRKFSKDSGLRGLXOGFNVSVOG 182
 QY 183 IIVYRAAYEGYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSG 242
 DB 183 IIVYRAAYEGYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSG 242
 QY 243 RKGADIMYGTGDCNRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKY 297
 DB 243 RKGADIMYGTGDCNRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKY 297
 RESULT 13
 ID 09H0C2 PRELIMINARY; PRT; 315 AA.
 AC 09H0C2;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE HYPOTHETICAL 35.0 KDA PROTEIN.
 GN DKFZP434N1235.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AL136857; CAB66791.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carf; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 1.
 KW Hypothetical protein; Inner membrane; Mitochondrion; Transmembrane;
 KW Transport. 315 AA; 35022 MW; 9ACE26062CC9675 CRC64;
 SO SEQUENCE

Query Match 70.9%; Score 1101.5; DB 4; Length 315;
 Best Local Similarity 73.0%; Pred. No. 3.2e-93;
 Matches 214; Conservative 31; Mismatches 45; Indels 3; Gaps 2;

OY 5 AANFLKDLGAVAAVSTAVAPIERVKLLQVQHASQISAQKQYKGIIDCVRIPIRKE 64
 DB 17 AASFGDLGAGVAAVSTAVAPIERVKLLQVQHASQISAQKQYKGIIDCVRIPIR 76
 OY 65 QGFLSWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFRYRAGNLASGAAG 124
 DB 77 QGFFSWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFRYRAGNLASGAAG 136
 OY 125 AATLCVYVPLDPAKRTPLADVGR-RAOREPHGDCIIRKFSQDGLRGTYOGFNVSGI 183
 DB 137 AATLCVYVPLDPAKRTPLADVGR-RAOREPHGDCIIRKFSQDGLRGTYOGFNVSGI 196
 OY 184 IYRAAYFGVYDPAKGMPLDPKRVHIFVSMIAQSVTAAGLSTYFPTVRRMMQSGR 243
 DB 197 IYRASYFGVYDPAKGMPLDPKRVHIFVSMIAQSVTAAGLSTYFPTVRRMMQSGR 256
 OY 244 KGAADIYTGTVDCWKRIADDEGAKAFKGAWSNVLRMGAGFVLYYDEIKKY 296
 DB 257 -AKROYKGTLDCAVKIIRNEGMSAMFKGALSNVFRGTGALVALYDEIKKY 307

RESULT 14
 ID P91410 PRELIMINARY; PRT; 313 AA.
 AC P91410;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO ADP/ATP TRANSLOCASE.
 GN T01B11.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Steliyes L.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: U80931; AAB38001.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carf; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 KW SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;
 SO SEQUENCE

Query Match 67.3%; Score 1045.5; DB 5; Length 313;
 Best Local Similarity 69.8%; Pred. No. 4.4e-88;
 Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;

OY 8 FLKDLGAVAAVSTAVAPIERVKLLQVQHASQISAQKQYKGIIDCVRIPIRKE 67
 DB 25 FLIDLASGTAATAVSTAVAPIERVKLLQVQHASQISAQKQYKGIIDCVRIPIRKE 84
 OY 68 LSWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFRYRAGNLASGAAGTS 127
 DB 85 AALMRGNLANVIRFPTQALNFAFKDKYKQLFLGVDNRHKOFRYRAGNLASGAAGTS 144
 OY 128 LCFVYVPLDPAKRTPLADVGRRAOREPHGDCIIRKFSQDGLRGTYOGFNVSGIIT 187
 DB 145 LCFVYVPLDPAKRTPLADVGRANERERKGLADCLVTKASGPIGLRGFVSVQGIIT 204
 OY 188 AAYFGVYDPAKGMPLDPKRVHIFVSMIAQSVTAAGLSTYFPTVRRMMQSGRGA 246
 DB 205 AAYFGVYDPAKGMPLDPKRVHIFVSMIAQSVTAAGLSTYFPTVRRMMQSGRGA 262
 OY 247 DIMYTGTVDCWKRIADDEGAKAFKGAWSNVLRMGAGFVLYYDEIKKY 297
 DB 263 DVLTKNTLDCAVKIIRNEGMSAMFKGALSNVFRGTGALVALYDEIKKY 313

RESULT 15
 ID Q21103 PRELIMINARY; PRT; 313 AA.
 AC Q21103;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE K01H12.2 PROTEIN.
 GN K01H12.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC McMurray A.;
 RA Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
 RL [2]

RP SEQUENCE FROM N.A.
 RA MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: Z68218; CA92472.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SO SEQUENCE 313 AA; 34384 MW; D1E435DB463C984 CRC64;

Query Match 67.2%; Score 1043.5; DB 5; Length 313;
 Best Local Similarity 69.4%; Pred. No. 6,8e-88;
 Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;

OY 8 ELKDFLAGAANAASKTAVAPIERVKLLQVQASQISAERQYKGIIDCVRIPEQGF 67
 || | : | ||||| ||||| || | : | : ||||| : ||||| :
 DB 25 FLIDLASGCTAAVASKTAVAPIERVKLLQVQASLTITADRKRYGIVDVLVRPEQGY 84
 : ||||| ||||| ||||| || : | : | : ||||| |||||
 OY 68 LSFNRGNLANVIRYPTQALNFAFKDKYKQLFGLGVDRHKQFWRFFAGNLASGAAGATS 127
 : ||||| ||||| ||||| || : | : | : ||||| |||||
 DB 85 AALWRGNLANVIRYPTQALNFAFKDTYKNIPQGLDKKDFWKEFAGNLASGAAGATS 144
 : ||||| ||||| ||||| || : | : | : ||||| |||||
 OY 128 LCFVYPLDFARTRLADVGRRAQREFHGLGDCIIRIFKSDGLRGLYQGFNVSVQGIITYR 187
 ||||| ||||| ||||| : ||| | : ||||| ||||| ||||| |||||
 DB 145 LCFVYPLDFARTRLADVGRKANEREFKGLADCLVIAKSDGPIGLYRGFFVSVQGIITYR 204
 ||||| ||||| ||||| : ||| | : ||||| ||||| ||||| |||||
 OY 188 AAYFGVYDTAKGML-PDPKRVHIEVSMIAQSVTAVAGLSTYPPDTVRRRRMMQSGRKGA 246
 ||||| : ||| : | : | : | : | : ||||| ||||| |||||
 DB 205 AAYFGMFDPAKRVFTADGKRLNFFAAMALAQVTVGSGIISYPMDFVRRRRMMQSGRK-- 262
 ||||| : ||| : | : | : | : | : ||||| ||||| |||||
 OY 247 DIMYTGTVDCMKRIAKDEGAKAFPGAGSNVLRGMGAFVLVLYDEIKKYV 297
 ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
 DB 263 DVLKNTLDCAVKITRNGSMAMFKGALSNVFRGTGALVLAIVDEIQKFI 313

Search completed: February 13, 2002, 09:34:14
 Job time: 171 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 : Search time 22.53 Seconds

(Without alignments)
483.331 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRMGAFVLVLEIRKKV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	1466.5	94.4	298	1 ADT1_RAT	Q05962 rattus norv
3	1457.5	93.9	298	1 ADT1_MOUSE	P48962 mus musculi
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51881 mus musculi
6	1407.5	90.6	298	1 ADT2_RAT	Q09073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P12207 bos taurus
10	1211	78.0	297	1 ADT1_DROME	Q26365 drosophila
11	1162.5	74.9	301	1 ADT1_ANOGA	Q27238 anopheles g
12	973.5	62.7	339	1 ADT1_CHLRE	P31692 chlorella k
13	770.5	49.6	308	1 ADT1_CHLRE	P27080 chlamydomon
14	756.5	48.7	357	1 ADT1_MAIZE	P04709 zea mays (m
15	752.5	48.5	322	1 ADT1_SCHPO	Q03188 schizosacch
16	752.5	48.5	322	1 ADT1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	1 ADT1_ORYSA	P16591 oryza sativ
18	751.5	48.4	382	1 ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	1 ADT1_WHEAT	Q41629 triticum ae
22	740	47.6	385	1 ADT2_SOLTU	P27081 solanum tub
23	737	47.5	385	1 ADT2_ARATH	P40941 arabidopsis
24	736	47.4	307	1 ADT3_YEAST	P18238 saccharomyc
25	734	47.3	318	1 ADT2_YEAST	P18239 saccharomyc
26	733.5	47.2	313	1 ADT1_NEUCR	P02723 neurospora
27	729	46.9	305	1 ADT1_KLULA	P49382 kluyveromyc
28	728.5	46.9	331	1 ADT2_WHEAT	Q41630 triticum ae
29	718.5	46.3	309	1 ADT1_YEAST	P47476 saccharomyc
30	300.5	19.3	678	1 CMCI_HUMAN	O75746 homo sapien
31	296.5	19.1	330	1 GDC_BOVIN	O61888 bos taurus
32	296.5	19.1	702	1 CMCI_CAEL	Q21133 caenorhabdl
33	296	19.1	588	1 CMCI_CAEL	Q20799 caenorhabdl

34	295	19.0	322	1 GDC_RAT	P16261 rattus norv
35	292.5	18.8	307	1 YOTL_YEAST	O99297 saccharomyc
36	292	18.8	332	1 GDC_HUMAN	P16260 homo sapien
37	291	18.7	675	1 CMCI_HUMAN	O99450 homo sapien
38	286	18.4	587	1 CMCI_CAEL	O19359 caenorhabdl
39	279.5	18.0	676	1 CMCI_MOUSE	O99454 mus musculi
40	267.5	17.2	322	1 BMCP_MOUSE	O92282 mus musculi
41	265.5	17.1	325	1 BMCP_HUMAN	O92258 homo sapien
42	263.5	17.0	695	1 CMCI_DROME	O99473 drosophila
43	258.5	16.6	326	1 YEOU_SCHPO	O13805 schizosacch
44	248.5	16.0	324	1 PWT_YEAST	P32332 saccharomyc
45	246	15.8	436	1 BTL_MAIZE	P29518 zea mays (m

ALIGNMENTS

RESULT 1	ADT1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP			
DE	TRANSLUCASE 1) (ADENINE NUCLEOTIDE TRANSLUCATOR 1) (ANT 1).			
GN	SIC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:89236396; PubMed:2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial			
RT	ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:89340499; PubMed:2547778;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.;			
RA	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons,			
RT	it is located on chromosome 4, and is differentially expressed.";			
RT	J. Biol. Chem. 264:13998-14004(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:88041149; PubMed:2823266;			
RA	Neckermann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack			
RT	of a leader peptide, divergence from a fibroblast translocator cDNA,			
RT	and coevolution with mitochondrial DNA genes.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).			
RN	[4]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RC	TISSUE: Liver;			
RX	MEDLINE:88124845; PubMed:2829183;			
RA	Houldsworth J., Attard G.;			
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA			
RT	level in adult human liver.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).			
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE			
CC	MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL			
CC	INNER MEMBRANE.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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 CC or send an email to license@sib-sib.ch).

DR EMBL, J02966; AAA61223.1; -
 DR EMBL, J03593; AAA36751.1; -
 DR EMBL, J04982; AAA51736.1; -
 DR PIR, A28116; A28116.
 DR PIR, A39891; A39891.
 DR PIR, S03893; S03893.
 DR PIR, A44778; A44778.
 DR MIM, I03220; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; ADPTRNSLCASE.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; Mitoch_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA: 33064 MW: 59F0DFAECAETGCFBB CRC64;

Query Match 98.3%; Score 1526.5; DB 1; Length 298;

Best Local Similarity 98.3%; Pred. No. 1.8e-131;
 Matches 293; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
 QY 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 DB 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 QY 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 DB 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 179
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 180
 QY 180 VGGIITIRAYAGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSPFTVRRRMM 239
 DB 180 VGGIITIRAYAGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSPFTVRRRMM 239
 QY 240 OSGRKADIMYGTVCWCKRIAKDEGAKAFKFGAMSNVLRGSGAVLVLYDEIKKYV 297
 DB 240 OSGRKADIMYGTVCWCKRIAKDEGAKAFKFGAMSNVLRGSGAVLVLYDEIKKYV 297

RESULT 2

ADT1_RAT STANDARD; PRT; 298 AA.
 AC 005962;
 DT 01-FEB-1994 (Rel. 28. Created)
 DT 01-FEB-1994 (Rel. 28. Last sequence update)
 DT 20-AUG-2001 (Rel. 40. Last annotation update)
 DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
 DE TRANSLCASE 1) (ADENINE NUCLEOTIDE TRANSLCATOR 1) (ANT 1).
 GN SIC3544 OR ANT1.
 OG Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY, AND WISTAR, TISSUE-Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozaki Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC - SUBUNIT: HOMODIMER.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC - TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).

DR EMBL, X61667; CAA43842.1; -
 DR EMBL, D12770; BAA02237.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; ADPTRNSLCASE.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA: 32989 MW: 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;

Best Local Similarity 94.3%; Pred. No. 5.1e-126;
 Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
 DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
 QY 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 DB 61 IPKEGFLSFMWGNLANVIRYPTQALNFAFDKQKQLFLGVDNRHKKQWRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 179
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREPHGLGDCIIRKFSDDLRLGYGFNV 180
 QY 180 VGGIITIRAYAGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSPFTVRRRMM 239
 DB 180 VGGIITIRAYAGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSPFTVRRRMM 239
 QY 240 OSGRKADIMYGTVCWCKRIAKDEGAKAFKFGAMSNVLRGSGAVLVLYDEIKKYV 297
 DB 240 OSGRKADIMYGTVCWCKRIAKDEGAKAFKFGAMSNVLRGSGAVLVLYDEIKKYV 297

RESULT	3
ADTL_MOUSE	
ID	ADTL_MOUSE
STANDARD:	PRT: 298 AA.
AC	P49862;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1);
GN	SLC25A4 OR ANT1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=97059403; PubMed=8903724;
RA	Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT	"Rapid evolution of human pseudautosomal genes and their mouse homologs.";
RL	Mamm. Genome 7:25-30(1996).
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC	-1- SUBUNIT: HOMODIMER.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: U27315; AAC52837.1; -.
DR	MGD: MGI:1353495; Slc25a4.
DR	InterPro: IPR002067; Mit_carrier.
DR	InterPro: IPR001993; Mitoch_carrier.
DR	Pfam: PF00153; mltc_carr; 3.
DR	PRINTS: PR00926; MITOCARRIER.
DR	PRINTS: PR00927; ADPTRNSLCASE.
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family.
KW	-----
FT	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 110 1.
FT	REPEAT 111 208 2.
FT	REPEAT 209 298 3.
FT	REPEAT 298 32870 MM; 32AC3B4EFCFA482 CRC64;
SO	SEQUENCE
Query Match	93.9%; Score 1457.5; DB: 1; Length 298;
Best Local Similarity	93.6%; Pred. No. 3.4e-125;
Matches 279;	Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY	1 MGDHMSFLKDFLAGAVALAAVSKTAVAPLERKLLQVQHASKQISAERKQYGIIDCVVR 60
DB	1 MGDQALSLFKDPLAGLGGIAAAVSKTAVPIERKLLQVQHASKQISAERKQYGIIDCVVR 60
OY	61 IPKDGFLSFWNGNLANYIRFPOTALNFAFDKTKKOLFGLGVDRHKQFWRYPAGNLASG 120
DB	61 IPKDGFLSFWNGNLANYIRFPOTALNFAFDKTKKOLFGLGVDRHKQFWRYPAGNLASG 120

```

Oy 121 GAGGTGTCFCFYVPLDFAFTRRLAAOVGR - RAQREHFGLGDCIIKFKSGKLGVLVOGFNVS 179
Db 121 GAAAGTSTLCFCYVPLDLARFLARLAAADVGKSSQREFFGLGDLCKLFKFSGLKGLGVGFVS 180
Oy 180 VGGITTYEAAAFGVYDTRAKKMLPDKRVNHIEFYSWMIQAOSVTAVALGILSYPEFTVRRRMM 239
Db 181 VGGITTYEAAAFGVYDTRAKKMLPDKRVNHIIYSWMIQAOSVTAVALGILSYPEFTVRRRMM 240
Oy 240 QSGRGADIMYTGTVDCMRKIAKDEGANAFFKGSANVLRGGAFAVLVLYDEIKKYV 297
Db 241 QSGRGADIMYTGTVDCMRKIAKDEGANAAFFKGSANVLRGGAFAVLVLYDEIKKYV 298

RESULT 4
ADTL_BOVIN STANDARD: PRT: 297 AA.
ID ADTL_BOVIN
AC P02722:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Agulla H., Mista D., Bulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 297-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -I- SUBUNIT: HOWDIMER.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XWBO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mltch_carrier.

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DR Pfam: PF00153; mito_carr: 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER: 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Methylation.
 FT INIT_MER 0 0
 FT MOD_RES 1 1 BLOCKED.
 FT MOD_RES 51 51 METHYLATION (POTENTIAL).
 FT TRANSMEM 11 28 1 (POTENTIAL).
 FT TRANSMEM 72 90 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 175 194 4 (POTENTIAL).
 FT TRANSMEM 213 230 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 207 2.
 FT REPEAT 208 297 3.
 FT SEQUENCE 297 AA: 32836 MW: A582D3C4A40AEB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
 Best local Similarity 94.6%; Pred. No. 7.8e-125;
 Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 3 DHANSLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAERKQKGIIDCVVRIP 62
 DB 2 DQALSLKDFLAGGVAASIKSTAVADIERVKLLQVQHASKOISAERKQKGIIDCVVRIP 61
 OY 63 KKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRPFAGNLASGA 122
 DB 62 KKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRPFAGNLASGA 121
 OY 123 AGATSLCFVYPLDFARTRLAADVGR-AQREFFGLDCIIRKISGRLGYGFNVSVQ 181
 DB 122 AGATSLCFVYPLDFARTRLAADVGR-AQREFFGLDCIIRKISGRLGYGFNVSVQ 181
 OY 182 GIITTAATFCGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLVSPEDTVRRMMMS 241
 DB 182 GIITTAATFCGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLVSPEDTVRRMMMS 241
 OY 242 GRRGADIMTGTVDCKRIAKDEGAKAFKGSNVLKRGAGFVVLVDLKKYV 297
 DB 242 GRRGADIMTGTVDCKRIAKDEGAKAFKGSNVLKRGAGFVVLVDLKKYV 297

RESULT 5
 ADP2_MOUSE STANDARD: PRT: 298 AA.
 AC P51881; 061311; (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADONINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
 GN SL25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs".
 RL Mamm. Genome 7:25-30(1996).
 RP [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=skeletal muscle;
 RA Sheldon J.G.;
 RA Thesis (1995), University of Cambridge, U.K.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Cosset P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC
 CC EMBL: U27316; AAC2838.1; -
 CC EMBL: U10404; AAL19009.1; -
 CC EMBL: X70847; CAA50196.1; -
 CC MGD: MGI:1353496; Slc25a5.
 DR InterPro: IPR002067; Mit_carr.
 DR InterPro: IPR001993; Mitoch_carr.
 DR Pfam: PF00153; mito_carr: 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER: 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA: 32931 MW: 0798E04B987EFE20 CRC64;

Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best local Similarity 89.6%; Pred. No. 9.5e-121;
 Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;

OY 1 MGHANSLKDFLAGAANAASKTAVADIERVKLLQVQHASKOISAERKQKGIIDCVVR 60
 DB 1 MTDAAVSFANDFLAGVAASIKSTAVADIERVKLLQVQHASKOISAERKQKGIIDCVVR 60
 OY 61 IPKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRPFAGNLASG 120
 DB 61 IPKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRPFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFFGLDCIIRKISGRLGYGFNVSV 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFFGLDCIIRKISGRLGYGFNVSV 180
 OY 180 VCGIITTAATFCGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLVSPEDTVRRMMMS 239
 DB 181 VCGIITTAATFCGYVDTAKGMLPDKNVHIFVSMIAQSVTAAGLVSPEDTVRRMMMS 240
 OY 240 QSGRGADIMTGTVDCKRIAKDEGAKAFKGSNVLKRGAGFVVLVDLKKYV 296
 DB 241 QSGRGADIMTGTVDCKRIAKDEGAKAFKGSNVLKRGAGFVVLVDLKKYV 297


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RESULT 6
ADP2_RAT
ID ADT2_RAT STANDARD: PRT: 298 AA.
AC 009073:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
CC SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
CC BR EMBL: D12711; BAA02238.1; -
CC DR InterPro: IPR002067; Mlt_carrier.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr.3
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PRINTS: PR00927; ADPTRNSLOCASE.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
CC KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC Multigene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 111 1.
CC FT REPEAT 112 208 2.
CC FT REPEAT 209 298 3.
CC FT REPEAT 298 32901 MW; 6A59204B987EFC35 CRC64;
CC SEQUENCE
SQ

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Query Match          90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1,2e-120;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

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OY 1 MGDHANSFLKDLAAGVAAVSKTAAVPIERVLLQVQHASKOISAEKQGIIDCVR 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 1 MTDAAVSFAEDFLAGGAAIAISKTAAPIERVKLLQVQHASKOITADKQKGIIDCVR 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 61 IPEQGFSLWKNLANVIRFPTQALNFAFKKQYKQLFGVGRHKKOFRRYRAGNLASG 120
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 61 IPEQGVSLWKNLANVIRFPTQALNFAFKKQYKQIFLGVDKRTQGFWRYPAGNLASG 120
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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OY 121 GAAGATSLCFVYPLDFARTPLADVGR-AGREFHGLGDCIIKIFKSDGLRGLYOGPNVS 179
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 121 GAAGATSLCFVYPLDFARTPLADVGR-AGREFHGLGDCIIKIFKSDGLRGLYOGPNVS 180
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 180 VQGIIRYRAAFVGYDTAKMLDPPKRVHIFVSMIAQSVTAAGLLSYFDFVRRRMM 239
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 181 VQGIIRYRAAFVGYDTAKMLDPPKRVHIFVSMIAQSVTAAGLLSYFDFVRRRMM 240
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
OY 240 QSGRKAGDIWYGTVDCKRIADKGAFFKAGMSVNLGKGAFLVLYDEIKKY 296
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 241 QSGRKGTDIWYGTVDCKRIADKGAFFKAGMSVNLGKGAFLVLYDEIKKY 297
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
RESULT 7
ADT2_HUMAN
ID ADT2_HUMAN STANDARD: PRT: 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.";
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.-T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated.";
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.-N., Su Y., Baybayan P., Siruno A., Nagara R.,
RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozerisky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC EMBL; M57424; AAA51737.1; -
 CC EMBL; J02683; AAA35579.1; -
 CC EMBL; L78810; AAB39266.1; -
 CC EMBL; AC004000; AAB96347.1; -
 CC EMBL; J03591; AAA36749.1; -
 CC PIR; A29132; A29132.
 CC PIR; C28116; C28116.
 CC MIM; 300150; -
 CC InterPro; IPR002067; Mit_carrier.
 CC InterPro; IPR001993; Mitoch_carrier.
 CC Pfam; PF00153; mito_carr; 3.
 CC PRINTS; PR00926; MITOCARRIER.
 CC PRINTS; PR00927; ADPTRNSICASE.
 CC PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.

FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 7.7e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLAGAVAAVSKTAVAPIERYKLLQVQHASKQISAEROYGIIDCVVR 60
 DB 1 MDAVVSFAKDFLAGGVAIAISKTAVAPIERYKLLQVQHASKQITADQYGIIDCVVR 60
 OY 61 IPKEGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEGVSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDVDRHKQFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPPLDPFARRLADYGR-AOREPFGIGDCIIKIKRSQGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFVYPPLDPFARRLADYGR-AOREPFGIGDCIIKIKRSQGLRGLYOGFNVS 179
 OY 180 VOGIIYRAAYFGVYDTAKGMLPDPKRNVIHIVSMMIAQSVTAAGLSTYPTVRRMM 239
 DB 180 VOGIIYRAAYFGVYDTAKGMLPDPKRNVIHIVSMMIAQSVTAAGLSTYPTVRRMM 239
 OY 240 OSGRKGADIMTGTGTCFKRIKAKDCAKAFKFGANSNVLKRGGAFLVLYDEIKKY 296
 DB 241 OSGRKGTIDIMTGTGTCFKRIKAKDCAKAFKFGANSNVLKRGGAFLVLYDEIKKY 297

RESULT 8
 ADT3_HUMAN STANDARD; PRT; 298 AA.
 AC P12236;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP CARRIER PROTEIN, LIVER ISOFORM 12 (ADP/ATP TRANSLOCASE 3)
 GN SLC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A.; 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; J03592; AAA36750.1; -
 CC PIR; S03894; S03894.
 CC PIR; B28116; B28116.
 CC MIM; 300151; -
 CC MIM; 403000; -
 CC InterPro; IPR002067; Mit_carrier.
 CC InterPro; IPR001993; Mitoch_carrier.
 CC Pfam; PF00153; mito_carr; 3.
 CC PRINTS; PR00926; MITOCARRIER.
 CC PRINTS; PR00927; ADPTRNSICASE.
 CC PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.

FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 2).
 SQ SEQUENCE 298 AA; 32866 MW; 1B534E9F0E49672F CRC64;

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.2e-118;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLAGAVAAVSKTAVAPIERYKLLQVQHASKQISAEROYGIIDCVVR 60
 DB 1 MWDQAIISFAKDFLAGGIAIAISKTAVAPIERYKLLQVQHASKQITADQYGIIDCVVR 60
 OY 61 IPKEGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDVDRHKQFWRYPAGNLASG 120
 DB 61 IPKEGVSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDVDRHKQFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPPLDPFARRLADYGR-AOREPFGIGDCIIKIKRSQGLRGLYOGFNVS 179

	Matches	259;	Conservative	21;	Mismatches	17;	Indels	1;	Gaps	1,
Qy	1	MGDHAHSLKLPFLAGAVAAVSKTVAPIETRYKKLLLOVOHASKOISAEEKYKGIIIDCYVR	60							
Dd	1	MTEQAISFPAKFDELAGGIAAASIKSTVAADIERKKLLLOVOHASKOIQAOKYGYIDCIVR	60							
Oy	61	IPKEGFSLSPFRGNLANVIYRIFFPTQALNFAFDKTKYKOLFGLGVDRHKOFMRFFAGNLASG	120							
Dd	61	IPKEGGVLSPFRGNLANVIYRIFFPTQALNFARFKDKKQKFLFGVDKRTQFMRFAGNLASG	120							
Oy	121	GAAGATSLCEPVPLDFEAFTRLAADVGRR-AOREFHGLDCDIIRKFSOGLRGLYOGFNVS	179							
Dd	121	GAAGATSLCFYVPLDFEAFRTLAAADVKGSGSEREFGLDCLVKIRKSDGIRGLYOGFNVS	180							
Oy	180	VGGIIITAAAFEGVYDTAKGMPLDPKNHHIFPSMMIIAQSVTAVALLLSPPFTVRRRMNM	239							
Dd	181	VGGIIITAAAFEGVIDTKAGMLPDPKNHHIIVSMIIAQVTVAAGVSIPEFTVRRRMNM	240							
Qy	240	QSGRKGADIMYTGTVDCAKRRIAKDDGAKAFFGKAMSNVLRNGCAFVLYLVDIEIRKYV	297							
Dd	241	QSGRKGADIMYKGTVDCAKRRIILKDGGKAFFRGAMSNVLRNGCAFVLYLYDELKKVI	298							
RESULT	10									
ID	ADT_DROME	STANDARD:	PRT:	297	AA.					
AC	Q26365; Q26254; P91614; O9VZ70;									
DT	15-JUL-1998 (Rel. 36, Created)									
DT	15-JUL-1998 (Rel. 36, Last sequence update)									
DT	20-AUG-2001 (Rel. 40, Last annotation update)									
DE	ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE									
DE	TRANSLOCATOR) (ANT) (STRESS SENSITIVE B PROTEIN).									
GN	SEB OR A/A-T OR CG16944.									
OC	Drosophila melanogaster (Fruit fly).									
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;									
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;									
CC	Ephydroidea; Drosophilidae; Drosophila.									
OX	NCBI_TaxID=7227;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=92389367; PubMed=1387687;									
RA	Louvi A., Tsitlilou S.G.;									
RT	"A cDNA clone encoding the ADP/ATP translocase of Drosophila									
RT	melanogaster shows a high degree of similarity with the mammalian									
RT	ADP/ATP translocases.";									
RL	J. Mol. Evol. 35:44-50(1992).									
RN	[2]									
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=94350065; PubMed=7520869;									
RA	Hutter P., Karch F.;									
RT	"Molecular analysis of a candidate gene for the reproductive									
RT	isolation between sibling species of Drosophila."									
RT	Experientia 50:749-762(1994).									
RN	[3]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN=ORECON-R;									
RA	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;									
RA	Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.									
RN	[4]									
RP	SEQUENCE FROM N.A.									
RC	STRAIN-BERKELEY;									
RA	Medline=20196006; Pubmed=10731132;									
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,									
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,									
RA	George R.G., Lewis S.E., Richards S.C., Ashburner N., Henderson S.N.,									
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,									
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champé M., Pfeiffer B.D.,									
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,									
RA	Abbill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,									
RA	Ballew R.M., Basay A., Baxendale J., Bayraktaroglu L., Beasley E.M.,									

RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jaislin M., Jalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattle B., McInosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon R., Nussaker D.R., Pacle J.M.,
 RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Schelder F., Shen H.,
 RA Shue B.C., Sildenafilimos I., Stimpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Glods R.A., Myers E.W., Rudin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC
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 CC -----
 DR EMBL: S43651; AAB23114.1; -.
 DR EMBL: S71762; AAB31734.3; -.
 DR EMBL: Y10618; CAJ71628.1; -.
 DR EMBL: AE003484; AAF47957.1; -.
 DR FlyBase: FBgn0003360; seqs.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitochl_carrier.
 DR Pfam: PF00153; mltc_carri; 3-
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; inner membrane; Repeat; Transmembrane; Transport.
 FT FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT CONFLICT 18 19 OV -> GI (IN REF. 3 AND 4).
 FT CONFLICT 81 81 I -> Y (IN REF. 1).
 FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
 FT CONFLICT 266 266 G -> A (IN REF. 2).
 FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT CONFLICT 268 268 C -> S (IN REF. 1).
 QO SEQUENCE 297 AA; 32880 MW; AA639433968F9750 CRC64;

Query Match	78.0%	Score 1211;	DB 1;	Length 297;
Best Local Similarly	79.4%	Pred. No. 8.3e-103;		
Matches 231; Conservative	25;	Mismatches 33;	Indels 2;	Gaps 2;

QY	5	AMSEFKDPLAAGVAANAASKTAVAPLEPERKLLLOVQHASKQISAEOKYGIIIDCVARIKE	64
Dd	7	AVGFPEKDPAAGVSAANSAVKTAVPATIERKKLLLOVHISKQISPDCKOYGMDCFIIRIKE	66
QY	65	OGLTFSEWGNLANVIRYPTPOLNAFNFADKYKOLFUGVDVRHRKOFWRYPAGNLASGGAAG	124
QY	125	ATSLCFEVPDPARFLAADYGRAROREFHIGDCIIRIKFSDDGRJGYOGPNNSVOGIT	184
Dd	127	ATSLCFEVPDPARFLAADYGRAROREFHIGDCIIRIKFSDDGVGLYRGFGVSQGII	186
QY	185	IYRAAFEGVDTAKMGLPDKPVNHIEFVSMIAQSATAAGLSLTFEDTVRRMMQSGRK	244
Dd	187	IYRAAFEGVDTAR-MLPDPKNTPYISMALTAQQVTYTAGIVSPFDVIRRRMMQSGRK	245
QY	245	GADIMYTGTVDCKRIAKDEGAKAEFFKGAMSNVLRMGCAFVLVLYDEIKK	295
Dd	246	ATEVIYKNTLHCMTIAKQEG-PCFEFKAFSNIILRGTAFAVLVLYDEIKK	295
 RESULT 11 ADT_ANGOA STANDARD; PRT; 301 AA.			
ID	ADT_ANGOA	STANDARD;	PRT; 301 AA.
AC	027238:		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	ADP_CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT).		
OS	Anopheles gambiae (African malaria mosquito).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Euryptera; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.		
OX	NCBI_TaxID=7165;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-G3:		
RX	MEDLINE=94348635; PubMed=8069414;		
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;		
RT	"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae."		
RL	Insect Mol. Biol. 3:35-40(1994).		
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
CC	-----		
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CC	-----		
DR	EMBL; L11618; AB04104.1; -		
DR	EMBL; L11617; AB04105.1; -		
DR	InterPro: IPR002067; Mlt_carrier.		
DR	InterPro: IPR001993; Mitoch_carrier.		
DR	Pfam; PF00153; mltc_carr; 3.		
DR	PRINTS; PR00926; MITOCARRIER.		
DR	PRINTS; PR00927; ADPTRNSLCASE.		
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.		
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.		
FT	TRANSMEM 14 31 1 (POTENTIAL).		
FT	TRANSMEM 75 93 2 (POTENTIAL).		
FT	TRANSMEM 119 136 3 (POTENTIAL).		
FT	TRANSMEM 178 197 4 (POTENTIAL).		


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DR EMBL: X65194; CAA46311.1; -.
DR PIR: S30259; S30259.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 2.
DR Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport.
KW TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.6%; Score 770.5; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 8,9e-63;
Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;

OY 7 SFLKDFLAGAANAASKTAVAPIERVKLLLOVO-HASKQISAKEYKGIIDCVRIPEQ 65
DB 7 NMWDFLAGLSAASVSKTAAPIERVKLLIQNDEMIKQGRLASPKGIGCFVRIPEE 66
OY 66 GFLSFRGNLANVIRYEPYQALNFAFKDKYKQLFLGVDHRHQFWRYPAGNLSGGAAGA 125
DB 67 GGSILMRGNLTAVIRYEPYQALNFAFKDKRMF--GFKDKKEYWKMFGNMSGGAAGA 124
OY 126 TSLCEVYPLDFEARTLADVGR---AOREFHGLDCLIKFKSGGLGLYOGFVNSVO 181
DB 123 VLSLFFVYSLDVARTRLANAKSAKGGGDRQFGLVDVYRKTIASGLVGRFNIQCV 184
OY 182 GIIIRAAAFEGYDTAKG-MLPDPKNVHIFVSMIAOSVTAAGLISGPFDTVRRMMQ 240
DB 185 GIVVRGRLYFGVYDLSKPLVGLPLANNFLAFLGLGWITTAGLASVYIDIRRMWMT 244
OY 241 SGRKADIMYTTGVDCWRKIADEGAKAFKGAWSNVLRGMGAFVLYLDEI-----K 294
DB 245 S---GSAYVYNSFFHCFOIVNKGKSLFKGANILRAVAGVLAGYDOLQVILLGK 301
OY 295 KY 296
DB 302 KY 303

RESULT 14
ADTL_MAIZE STANDARD: PRT: 387 AA.
AC P04709;
DE 13-AUG-1987 (rel. 05, Created)
DE 01-AUG-1992 (rel. 23, Last sequence update)
DE 20-AUG-2001 (rel. 40, Last annotation update)
DE ADP-ATP CARRIER PROTEIN 1, MITOCHONDRIAL PRECURSOR (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN ANT1 OR ANT-G1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Poaceae; Andropogoneae; Zea.
OC NCBI_TaxId=4577;
OX
RN NCBI [1]
RN SEQUENCE FROM N.A.
RN STRAIN=MUTIND-FR7205034;
RX MEDLINE-91322533; PubMed-1863785;
RT "Winning B.M., Day C.D., Sarah C.J., Leaver C.J.";
RT "Nucleotide sequence of two cDNAs encoding the adenine nucleotide
RT translocator from Zea mays L.";
RN RL Plant Mol. Biol. 17:305-307(1991).
RN (2)
RN RP SEQUENCE OF 59-387 FROM N.A.
RN STRAIN=CV. B37N;

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RX MEDLINE-89338399; PubMed-2547608;
RA Leaver C.J., Bathgate B., Baker A.;
RT "Two genes encode the adenine nucleotide translocator of maize
RT mitochondria. Isolation, characterisation and expression of the
RT structural genes.";
RL Eur. J. Biochem. 183:303-310(1989).
RN (3)
RN SEQUENCE OF 70-387 FROM N.A.
RX MEDLINE-85297781; PubMed-2994015;
RA Baker A., Leaver C.J.;
RT "Isolation and sequence analysis of a cDNA encoding the ATP/ADP
RT translocator of Zea mays L.";
RL Nucleic Acids Res. 13:5857-5867(1985).
CC -i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -i- SUBUNIT: HOMODIMER.
CC -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: X57556; CAA40781.1; -.
DR EMBL: X15711; CAA33742.1; -.
DR EMBL: X02842; CAA26600.1; -.
DR PIR: A24072; A24072.
DR PIR: S05199; S05199.
DR PIR: S14876; S14876.
DR MaizeDB: 17145; -.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 2.
KW Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT CHAIN 1 77 MITOCHONDRION.
FT TRANSMEM 78 387 ADP-ATP CARRIER PROTEIN 1.
FT TRANSMEM 91 108 1 (POTENTIAL).
FT TRANSMEM 153 171 2 (POTENTIAL).
FT TRANSMEM 196 213 3 (POTENTIAL).
FT TRANSMEM 257 276 4 (POTENTIAL).
FT TRANSMEM 296 313 5 (POTENTIAL).
FT TRANSMEM 352 370 6 (POTENTIAL).
FT TRANSMEM 102 102 K -> E (IN REF. 2).
FT CONFLICT 154 154 N -> Y (IN REF. 3).
SQ SEQUENCE 387 AA; 42391 MW; DE73BB0F478BD57D CRC64;

Query Match 48.7%; Score 756.5; DB 1; Length 387;
Best Local Similarity 53.8%; Pred. No. 2,2e-61;
Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;

OY 7 SFLKDFLAGAANAASKTAVAPIERVKLLLOVO-HASKQISAKEYKGIIDCVRIPEQ 65
DB 86 NMIDPFMGVSAASVSKTAAPIERVKLLIQNDEMIKSGRLSEPKGIIDCFKRTIDE 145
OY 66 GFLSFRGNLANVIRYEPYQALNFAFKDKYKQLFLGVDHRHQFWRYPAGNLSGGAAGA 125
DB 146 GFSLSMRGNLTAVIRYEPYQALNFAFKDKRFGKRLNFKDR-DGYWKMPAGNLSGGAAGA 204
OY 126 TSLCEVYPLDFEARTLADVGR---AOREFHGLDCLIKFKSGGLGLYOGFVNSVOG 182
DB 205 SLSLFFVYSLDVARTRLANAKSAKGGGDRQFGLVDVYRKTIASGLVGRFNIQCVG 264

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QY 183 IIYRAVEGVYDTAK-----GMLPDKNVHIFVSMIAQSVTAVALGLSPEDTVRRM 237
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 265 IIYRGIFELVYSIKFVLTGNLD-----NFFASFLGMLITNGAGLAPIDTVRRM 320
QY 238 MMSGRRGADIMYTGTVDCMRKIAKDEGAKAFKGSANVLKMGCAFVLVYDEI---- 293
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 321 MMSGRA---VKYKSSLDAPQQLIKKKGPKSLFKGAGANILRAIAGAGVLSGVDOQLIF 377
QY 294 --KKY 296
  ||:|
Db 378 FGKKY 382

RESULT 15
ADT_SCHPO STANDARD; PRT; 322 AA.
ID ADT_SCHPO STANDARD; PRT; 322 AA.
AC 009188;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ADP ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
  TRANSLOCATOR) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Cousin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT *Cloning of the gene encoding the mitochondrial adenine nucleotide
  carrier of Schizosaccharomyces pombe by functional complementation in
  Saccharomyces cerevisiae.*;
RL Gene 171:113-117(1996).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
  Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
  MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: Z49974; CAA90275.1; -.
DR EMBL: AL023634; CAA19176.1; -.
DR HSSP: P04002; IATP.
DR InterPro: IPR002067; Mit_Carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 111 1
FT TRANSMEM 93 151 2
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 242 5 (POTENTIAL).

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FT TRANSMEM 289 309 6 (POTENTIAL).
SQ SEQUENCE 322 AA; 35020 MM; 8AC3D16A40F41AFC CRC64;

Query Match 48.5%; Score 752.5; DB 1; Length 322;
Best Local Similarity 52.9%; Pred. No. 4e-61;
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;

QY 7 SFLKDFLAGAVAAVSTAVAPIERVKLLQVOHASKOISAER---QYKIIDCVARIPK 63
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 26 TFFEDFMMGGVSAVSKTAAAPIERVKLLIQNQ---DEMIRAGRLSHRYKIGECFKRTAA 83
QY 64 EOGFLSPMRCNLNANVIRYPTQALNFAFKDKYKQFLGVDVRHKQFMRYPAGNLAGGAA 123
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 84 EGVYISLMRGNTANVLYRFTQALNFAFKDKYKQFLGVDVRHKQFMRYPAGNLAGGAA 142
QY 124 GATSLCFVYPLDFARTRLAAD---VGRRAOREFHGLDCIIRKSDGLRGLYOGFNVSV 180
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 143 GAASLLEFVYSLDYARTRLANDAKSARKGGERQFGLVDYVRKTYRSDGLRGLYRFGFSPV 202
QY 181 QGIIYRAATFGVYDTAKG-MLEDPKNVHIFVSMIAQSVTAVALGLSPEDTVRRMM 239
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 203 VGIVYVRGLYFGVDTLKPVVLGPLEGNFLASFLGMAVTTGSGVASYPELDTIRRRMM 262
QY 240 QSGRRGADIMYTGTVDCMRKIAKDEGAKAFKGSANVLKMGCAFVLVYDEIK 294
  ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 263 TSGEA---VKYSSFECCROIKAKEGARSEFKGAGANILGAGVLSITVDYO 314

```

Search completed: February 13, 2002, 09:34:42
Job time: 199 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 ; Search time 34.78 Seconds
(without alignments)
650.484 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRGMGAFLVLYDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP, ATP carrier pr
2	1466.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	2 S37210	ADP, ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP, ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP, ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP, ATP carrier pr
7	1380.5	88.9	298	2 B43646	ADP, ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP, ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP, ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23307	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	993.5	62.7	339	2 A41677	ADP, ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP, ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP, ATP carrier pr
18	756.5	48.7	322	2 S14876	ADP, ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP, ATP carrier pr
20	752.5	48.5	322	2 T09709	ADP, ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP, ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP, ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP, ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP, ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP, ATP carrier pr
27	740	47.6	379	2 S21313	ADP, ATP carrier pr
28	740	47.6	386	2 S14874	ADP, ATP carrier pr
29	737	47.5	385	1 S29852	ADP, ATP carrier pr

30	736	47.4	307	2 A36582	ADP, ATP carrier pr
31	734	47.3	318	1 A31978	ADP, ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP, ATP carrier pr
33	729	46.9	305	2 S68154	ADP, ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP, ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP, ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP, ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1
A44778
ADP, ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP, ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence, revision 17-Mar-2000 #text, change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989
A>Title: A human muscle adenine nucleotide translocator gene has four exons, its local
A:Reference number: A44778; M0ID:89340499
A:Accession: A44778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; M0ID:q178658; P0IDN:AAA51736.1; P0ID:q178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; M0ID:8926396
A:Accession: S03893
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A>Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; M0ID:88041149
A:Accession: A39891
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; M0ID:q339919; P0IDN:AAA61223.1; P0ID:q339920
R:Holdsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; M0ID:88124845
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOV>
A:Cross-references: GB:J03593; M0ID:q339724; P0IDN:AAA36751.1; P0ID:q339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-296/Product: ADP, ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 9.8e-131;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
DB 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
QY 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
DB 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
QY 180 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 239
DB 180 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 240
QY 240 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 2

160173

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: I60173

R:Shinozuka, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochem. Biophys. Acta 1152, 193-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: I60173; MUID:94002161

A:Accession: I60173

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA3842.1; PID:9400427

C:Genetics:

A:Gene: ancl

A:Introns: 37/3; 200/1; 247/1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;
Best Local Similarity 94.3%; Pred. No. 2.7e-125;

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
DB 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
QY 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
DB 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
QY 180 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 239
DB 181 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 240

QY 240 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 3

S37210

ADP,ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <LAP>

A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628

C:Genetics:

A:Gene: ANCI

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;
Best Local Similarity 94.0%; Pred. No. 5e-125;

Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
DB 1 MGDHMSFLKDLFLAGAVAAVSKTAVAPIERVKLLQVQHASKQISAERKYGIIIDCVVR 60
QY 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
DB 61 IPKEGGFLSPFMGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDPARTRLAADVGR--RAOREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
QY 180 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 239
DB 181 VOGIIITRAAYGVYDTAKGMLPDPKKNVHIFVSWMIAQSVTAAGLISYFPDTRRRMM 240
QY 240 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 OSGRKGADIMYGTVDCKWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 4

XHBO

ADP,ATP carrier protein T1 - bovine

N:Alternate names: ADP,ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C:Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mtochondrial ADP/ATP translocase expressed differently

A:Reference number: A43646; MUID:89229093

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <POM>

A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415

A:Rasmussen, U.B.; Wohlirab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unus

A:Reference number: A24822; MUID:86295775

A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RMS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mistr, D.; Bullitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267
 A:Accession: A03181
 A:Molecule type: Protein
 A:Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298' <ACU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Machter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82046808
 A:Accession: A61343
 A:Molecule type: Protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A:Reference number: S69369; MUID:95172058
 A:Accession: S69369
 A:Molecule type: Protein
 A:Residues: 49-63;154-168 <OET>
 A:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

* Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 1.4e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDAHSLKDFLAGAANAASKTAVAPTRVLLQVQHASQISAEKQKGLIDCVVR 60
 DB 1 MSQALSPKDFLAGAANAISKTAVAPTRVLLQVQHASQISAEKQKGLIDCVVR 60
 QY 61 IPKEQGLFSWRGNLANVIRFPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASC 120
 DB 61 IPKEQGLFSWRGNLANVIRFPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASC 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 180
 QY 180 VQGIITIRAYFEVYDTAKMGLPDPKKNVHIFVSMIAQSTAAVAGLTSYFDFVRRMM 239
 DB 181 VQGIITIRAYFEVYDTAKMGLPDPKKNVHIFVSMIAQSTAAVAGLTSYFDFVRRMM 240
 QY 240 QSGRKADIVYTGTVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 297
 DB 241 QSGRKADIVYTGTVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 298

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #ext_cchange 17-Mar-2000
 C:Accession: A29132; C8116
 R:Batini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu
 A:Reference number: A29132; MUID:87166056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:9179246; PIDN:AAA35579.1; PID:9179247
 R:Houdsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', '67-110', 'L', '112-161', 'G', '163-298' <HOU>
 A:Cross-references: GB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
 A:Experimental source: Clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

* Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.6e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDAHSLKDFLAGAANAASKTAVAPTRVLLQVQHASQISAEKQKGLIDCVVR 60
 DB 1 MTDAALSFADFLAGAAISTKAVAPTRVLLQVQHASQITADKQKGLIDCVVR 60
 QY 61 IPKEQGLFSWRGNLANVIRFPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASC 120
 DB 61 IPKEQGLFSWRGNLANVIRFPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASC 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 180
 QY 180 VQGIITIRAYFEVYDTAKMGLPDPKKNVHIFVSMIAQSTAAVAGLTSYFDFVRRMM 239
 DB 181 VQGIITIRAYFEVYDTAKMGLPDPKKNVHIFVSMIAQSTAAVAGLTSYFDFVRRMM 240
 QY 240 QSGRKADIVYTGTVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 296
 DB 241 QSGRKADIVYTGTVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 297

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N:Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP,
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #ext_cchange 17-Mar-2000
 C:Accession: S03894; B28116
 C:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
 A:Reference number: S03893; MUID:89226396
 A:Accession: S03894
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Houdsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: B28116

F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

```
Query Match          58.2%; Score 904.5; DB 2; Length 301;
Best Local Similarity 58.3%; Pred. No. 2,2e-74;
Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

QY 7 SFLKDELAGVAAVAAVSKTAVAPIERVKLLIQVQHASKQISA--EKQYKGIIDCVRIPIKE 64
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 8 NFADFLMGISAIKSTVVTPIERVKMLIQTDISIPEIKSGQVERYSGLINCCKRVSK 67

QY 65 QGFLSFNRGNLANVIRYPTQALNFAFKDKYKOLFLGVDHRHKQFWRVYFAGNLASGGAAG 124
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 68 QGVLSLRGNVANVIRYPTQALNFAFKDKYKOLFLGVDHRHKQFWRVYFAGNLASGGAAG 126

QY 125 AFSLCFVYPLDFARTRLADVGRRARQREFHGLGDCIIRKSDGLRGLYOGFNVSVOGII 184
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 AISLLIVYPLDFARTRLASDVGRRARQREFHGLGDCIIRKSDGLRGLYOGFNVSVOGII 186

QY 185 IYRAATEGYVDTKKML-PDPKRVHIFVSWMLQSTAVAGLLSYEDTYRRRRMMQSGR 243
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKWAAVQSVTTLAGLISYPEDTYRRRRMMQSGR 246

QY 244 KG-ADIMYTGTVDCWRRIAKDEGAKAFKFGAGSNVLRGMGAFVLVLYDEIRKVV 297
   || :|| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 247 KGEETIQYNTICWIKILRNESFGKFGAGMANVIRGAGALVLYVYDELRKLI 301
```

Search completed: February 13, 2002, 09:32:07
Job time: 44 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 ; Search time 57.26 Seconds

(without alignments)
384.208 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDAWSEFLKDFLAGAVAAA.....LRKGAFVLVYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq_1101: *
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20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT: *
21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT: *
22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	21	AAV71031 Human adenine nucl
2	1553	100.0	297	22	AAU01198 Human adenine nucl
3	1457.5	93.9	298	19	AAW61169 Antil protein. Mus
4	1391.5	89.6	298	21	AAV71032 Human adenine nucl
5	1391.5	89.6	298	22	AAU01199 Human adenine nucl
6	1385.5	89.2	298	21	AAV71033 Human adenine nucl
7	1385.5	89.2	298	22	AAW39641 Human polypeptide
8	1385.5	89.2	298	22	AAU01200 Human adenine nucl
9	1385.5	89.2	323	22	AAW41427 Human polypeptide
10	746	48.0	346	21	AAW36577 Arabidopsis thalia
11	746	48.0	346	21	AAW37261 Arabidopsis thalia

12	746	48.0	346	21	AAW37264 Arabidopsis thalia
13	746	48.0	346	21	AAW38460 Arabidopsis thalia
14	746	48.0	363	21	AAW36576 Arabidopsis thalia
15	746	48.0	363	21	AAW37260 Arabidopsis thalia
16	746	48.0	363	21	AAW37263 Arabidopsis thalia
17	746	48.0	363	21	AAW38459 Arabidopsis thalia
18	746	48.0	381	21	AAW36575 Arabidopsis thalia
19	746	48.0	381	21	AAW37259 Arabidopsis thalia
20	746	48.0	381	21	AAW37262 Arabidopsis thalia
21	746	48.0	381	21	AAW38458 Arabidopsis thalia
22	746	48.0	992	21	AAW38672 Arabidopsis thalia
23	746	48.0	1009	21	AAW38671 Arabidopsis thalia
24	746	48.0	1027	21	AAW38670 Arabidopsis thalia
25	743	47.8	346	21	AAW17731 Arabidopsis thalia
26	743	47.8	363	21	AAW17730 Arabidopsis thalia
27	743	47.8	381	21	AAW17729 Arabidopsis thalia
28	734	47.3	386	22	AAW00106 ADP/ATP carrier pr
29	686	44.2	333	21	AAW06857 Arabidopsis thalia
30	686	44.2	350	21	AAW06856 Arabidopsis thalia
31	686	44.2	368	21	AAW06855 Arabidopsis thalia
32	682	43.9	330	21	AAW20658 Arabidopsis thalia
33	681	43.9	330	21	AAW39398 Arabidopsis thalia
34	651.5	42.0	306	21	AAW12916 Arabidopsis thalia
35	651.5	42.0	306	21	AAW16974 Arabidopsis thalia
36	646	41.6	291	21	AAW20659 Arabidopsis thalia
37	645	41.5	291	21	AAW39399 Arabidopsis thalia
38	636.5	41.0	291	21	AAW12917 Arabidopsis thalia
39	636.5	41.0	291	21	AAW16975 Arabidopsis thalia
40	577	37.2	249	21	AAW20660 Arabidopsis thalia
41	576	37.1	249	21	AAW39400 Arabidopsis thalia
42	574	37.0	263	21	AAW12918 Arabidopsis thalia
43	574	37.0	263	21	AAW16976 Arabidopsis thalia
44	570	36.7	312	21	AAW28188 Arabidopsis thalia
45	557	35.9	228	21	AAW28189 Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV71031	AAV71031 standard; Protein; 297 AA.
XX	
AC	AAV71031:
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANTL.
KW	Human: adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinsonian; cerebrotectic; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
OS	
XX	
XX	Homo sapiens.
PN	WO200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	
PR	08-SEP-1999; 99US-0393441.
XX	
XX	(MITO-) MITOKOR.
XX	

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 44; Page 172; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTI from human brain.
 XX
 SQ Sequence 297 AA:
 Query Match 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGIIIDCVR 60
 DB 1 mgdhmsflkdfllagaaaavsktavapiervklllqvhasqsaekygiidcvr 60
 QY 61 IPKEGFLSFWRGNLANYIRFPTQALNFAFKDKYKQFLGVDVDRHKQWRFAAGNLASG 120
 DB 61 lpkegflsfwrgnlanyirfptqalnfaefkdkyqflfgvdrhkqwrfaagnlasg 120
 QY 121 GAAGATSLCFVPLDFARTRLADYGRRAQREFHGLGDCIIRFKSDGLRGLYOGFNVSV 180
 DB 121 gaagatslcfvpldfartrladvgrraqrefhglgdcilrkfsdglrglyogfnsv 180
 QY 181 OGIIIRAAVFCGVYPTAKGMLPDPKNNHIFVSWMTAQSVTAVAGLSYPTDVRRRMMQ 240
 DB 181 ogiiiraaavgvyptakgmlpdpknnhifvswmtaqsvtavaglsyptdvrrrmmq 240
 QY 241 SGRKGADIMYTGTCWCRRIAKDEGAKAFKGAWSNVLRGMGAFVLYLYDEIKRYV 297
 DB 241 sgrkgadimytgvcwcrkiaekgafkgawsnvlrmgafvlylydeikryv 297

RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 KW Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX

OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Fritzer LG;
 PI Vellicelebi G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule
 XX
 PS Disclosure: Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA:
 Query Match 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGIIIDCVR 60
 DB 1 mgdhmsflkdfllagaaaavsktavapiervklllqvhasqsaekygiidcvr 60
 QY 61 IPKEGFLSFWRGNLANYIRFPTQALNFAFKDKYKQFLGVDVDRHKQWRFAAGNLASG 120
 DB 61 lpkegflsfwrgnlanyirfptqalnfaefkdkyqflfgvdrhkqwrfaagnlasg 120
 QY 121 GAAGATSLCFVPLDFARTRLADYGRRAQREFHGLGDCIIRFKSDGLRGLYOGFNVSV 180
 DB 121 gaagatslcfvpldfartrladvgrraqrefhglgdcilrkfsdglrglyogfnsv 180
 QY 181 OGIIIRAAVFCGVYPTAKGMLPDPKNNHIFVSWMTAQSVTAVAGLSYPTDVRRRMMQ 240
 DB 181 ogiiiraaavgvyptakgmlpdpknnhifvswmtaqsvtavaglsyptdvrrrmmq 240
 QY 241 SGRKGADIMYTGTCWCRRIAKDEGAKAFKGAWSNVLRGMGAFVLYLYDEIKRYV 297
 DB 241 sgrkgadimytgvcwcrkiaekgafkgawsnvlrmgafvlylydeikryv 297

RESULT 3

AAW61169 standard; Protein: 298 AA.

AAW61169;

28-SEP-1998 (first entry)

Anti protein.

Anti. Adenine nucleotide translocator; cloning; screening;

DNA Tag di-deoxy terminator cycle sequencing; oxidative phosphorylation;

probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

hyperrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;

lactic acidosis; degenerative muscle disease.

Mus sp.

MO9819714-A1.

14-MAY-1998.

31-OCT-1997; 97MO-US19882.

01-NOV-1996; 96US-0030017.

(UYEM-) UNIV EMORY.

Graham BC, Macgregor GR, Wallace DC;

N-PSDB; AAV36479.

MICE lacking heart-muscle adenine nucleotide translocator protein -

used as model for mitochondrial myopathy and hyperrophic

cardiomyopathy in animals and to test therapeutic compositions or

gene therapies

Disclosure: Page 39-40; 61pp: English.

The present sequence is the mouse Anti protein, the cDNA producing this

polypeptide is cloned by screening a mouse heart cDNA library with the

human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA

Tag di-deoxy terminator cycle sequencing. The Anti protein is encoded by

the Anti locus, a nuclear gene on chromosome 8. This protein is required

in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP

which can then be converted into ATP. An Anti homozygous mutant would

thus be defective in OXPHOS which results in disease in oxidative

metabolism dependent tissues. This mouse Anti homozygous mutant can be

used as a model system for fasciocalcular humeral muscular dystrophy,

hyperrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model

systems can be used to test possible therapeutic compounds which

increase/mediate ATP and ADP exchange across the mitochondrial membrane

Independent of Anti.

Sequence 298 AA:

SO.

Query Match 93.9%; Score 1457.5; DB 19; Length 298;

Best Local Similarity 93.6%; Pred. NO. 2.2e-162;

Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

1 MGDAWFLDPLAGAAVAVSTKAVAPTRERVKLLLOVHAQSIASEKQKGIIDCVR 60

1 mgdgaflldplagaaavstkaavptreervklllovhqasikasekqgkllidcvr 60

1 ipkqegflsfwrgnlavirfptqalnfafkdkykolflgvgvdrhmqofwrfaglnlasg 120

1 ipkqegflsfwrgnlavirfptqalnfafkdkykolflgvgvdrhmqofwrfaglnlasg 120

121 GAAGATSLCFYPLDFAKRLAADVGR-KAQRERHGLDCLIKFKSDGLGLYQGRNVS 179

121 gaagatslcfypldftakrlaadvggrkaqrerhglldclikfksgdglklyqgrfsvs 180

RESULT 4

AAV71032 standard; Protein: 298 AA.

AAV71032;

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT2.

Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;

adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;

mitochondrial permeability transition; neuroprotective; noctropic;

antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;

antipariatic; cerebroprotective; therapeutic; screening; psoriasis;

Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;

diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;

mitochondrial encephalopathy; lactic acidosis; stroke; MIDO;

mitochondrial diabetes and deafness; hyperproliferative disorder;

myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

WO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99MO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0393441.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;

Ghosh SS;

N-PSDB; AAD00520.

Recombinant construct encoding adenine nucleotide translocator

polypeptide, useful e.g. in screening for potential therapeutic agents

against mitochondrial disease

Claim 45; Page 172-173; 175pp: English.

The patent discloses a method to produce adenine nucleotide translocator

(ANT) proteins or ANT fusion proteins using recombinant expression

constructs. ANT is a nuclear encoded protein and a major component of

inner mitochondrial membrane. It mediates transport of adenosine

di/tri-phosphates across the mitochondrial inner membrane and also serves

as an important molecular component of the mitochondrial permeability

transition pore, a modulator of apoptosis. ANT is used to identify agents

or ligands that bind to, or interact with it. The ANT ligands are used to

detect or isolate ANT in a biological sample, and therapeutically for

regulating mitochondrial pore activity, for treating diseases associated

with altered mitochondrial function, including Alzheimer's, Parkinson's

and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,

Leber's hereditary optic neuropathy, schizophrenia, mitochondrial

encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

disorders, mitochondrial diabetes and deafness (MIDO), and myoclonic

epilepsy red ragged fibre syndrome. The present sequence is an

adenine nucleotide translocator ANT2 from human brain.

```

XX      SQ      Sequence      298 AA:
Query Match      89.6%; Score 1391.5; DB 21; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.2e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY      1 MGDHANSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKQISAERQYGIIDCVYR 60
DB      1 mtdaaistakdfliagvvaaisktavapiervklllvqhaskqltadkqygidcvvr 60
OY      61 IREQGFELSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRRKQWRFRAGNLASG 120
DB      61 lpekegevlstfwgnlanvlyrftqalnfafkdkyqkflfgvdkrtqwrfragnlaag 120
OY      121 GAAGATSLCFVYPLDFAPRRLADVGR-AQREFHGLGDCITIKFEKSDGLRGYGFNVNS 179
DB      121 gaagatslcfvypldfartclraadvagagaerefrlgdcivklysgdtklyggnvns 180
OY      180 VOGIITRYAAYEGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYPFDRRRMM 239
DB      181 vgililyraayfglydtakgmldpdknchlvswmlaqvtavagllsyppfdtrrrmm 240
OY      240 QSGRRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGAVLVLYDEIKRY 296
DB      241 qsgrrktdlmvgtldcwrkrlardegskafkfgawsnvlrmgagavlvlydeikry 297

RESULT 5
AAU01199
ID      AAU01199 standard; Protein; 298 AA.
AC      AAU01199;
XX      07-SEP-2001 (first entry)
DE      Human adenine nucleotide translocator-2 (ANT-2) protein.
XX      Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
KW      mitochondrial permeability transition pore component; cell survival;
KW      mitochondrial core component; mitochondrial related disorder; cancer;
KW      Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX      Homo sapiens.
XX      WO200132876-A2.
XX      10-MAY-2001.
XX      03-NOV-2000; 2000WO-US30535.
XX      03-NOV-1999; 99US-0434354.
XX      (MITO-) MITOKOR.
XX      Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI      Velicelebi G, Davis RE;
DR      WPI; 2001-291054/30.
DR      N-PSDB; AAS05902.
XX      New nucleic acid expression constructs, useful for screening for agents
PT      that alter mitochondrial permeability transition (MPT), comprises
PT      polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT      fused to energy transfer molecule -
XX      Disclosure; Fig 2; 186pp; English.
XX      The present sequence represents human adenine nucleotide translocator-2
CC      (ANT-2) protein. ANT proteins are mitochondrial permeability
CC      transition (MPT) pore components responsible for mediating transport
CC      of ADP across the mitochondrial inner membrane. ANT proteins interact

```

```

CC      with other mitochondrial core components e.g. cyclophilins to
CC      regulate MPT. The present invention relates to a novel nucleic acid
CC      expression construct comprising a promoter operably linked to a
CC      polynucleotide encoding a mitochondrial pore component polypeptide
CC      (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC      (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel
CC      expression construct can alter mitochondrial membrane permeability
CC      transition and/or alter the interaction between mitochondrial core
CC      components. The methods are useful for screening for agents that alter
CC      MPT and/or cell survival. These agents are useful for the prevention or
CC      treatment of diseases associated with altered mitochondrial function or
CC      dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC      mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC      mitochondrial encephalopathy, lactic acidosis, stroke,
CC      hyperproliferative disorders e.g. cancer, and deafness.
XX      XX

SQ      Sequence      298 AA:
Query Match      89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.2e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY      1 MGDHANSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKQISAERQYGIIDCVYR 60
DB      1 mtdaaistakdfliagvvaaisktavapiervklllvqhaskqltadkqygidcvvr 60
OY      61 IREQGFELSFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDKRRKQWRFRAGNLASG 120
DB      61 lpekegevlstfwgnlanvlyrftqalnfafkdkyqkflfgvdkrtqwrfragnlaag 120
OY      121 GAAGATSLCFVYPLDFAPRRLADVGR-AQREFHGLGDCITIKFEKSDGLRGYGFNVNS 179
DB      121 gaagatslcfvypldfartclraadvagagaerefrlgdcivklysgdtklyggnvns 180
OY      180 VOGIITRYAAYEGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYPFDRRRMM 239
DB      181 vgililyraayfglydtakgmldpdknchlvswmlaqvtavagllsyppfdtrrrmm 240
OY      240 QSGRRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGAVLVLYDEIKRY 296
DB      241 qsgrrktdlmvgtldcwrkrlardegskafkfgawsnvlrmgagavlvlydeikry 297

RESULT 6
AA71033
ID      AA71033 standard; Protein; 298 AA.
AC      AA71033;
XX      29-AUG-2000 (first entry)
DE      Human adenine nucleotide translocator ANT3.
XX      Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW      adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW      mitochondrial permeability transition; neuroprotective; neurotropic;
KW      antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW      antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW      Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW      diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW      mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW      mitochondrial diabetes and deafness; hyperproliferative disorder;
KW      myoclonic epilepsy red ragged fibre syndrome.
XX      Homo sapiens.
XX      WO2000026370-A2.
XX      11-MAY-2000.
XX      03-NOV-1999; 99WO-US25883.
XX

```


CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA338642-AA442213) with neurotropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotid
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX
XX Sequence 323 AA;

Query Match	89.2%;	Score 1385.5;	DB 22;	Length 323;
Best Local Similarity	87.2%;	Pred..No. 6.8e-154;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

RESULT	10
AAG36577	
ID	AAG36577 standard; Protein; 346 AA.

AC	AAG36577;
XX	
DT	18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44845.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0126264

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Query match	48.08; Score 746; DB 21; Length 346;
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AC	AAG37261:		
DT	18-OCT-2000	(first entry)	
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DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 45788.	
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KM	Protein identification: signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter		
XX	termination sequence.		
OS	Arabidopsis thaliana.		

XX EP103405-A2.
PN
XX
XX 06-SEP-2000.
PD
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PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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DT	18-OCT-2000	(first entry)
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XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter	
XX	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
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PR	25-FEB-1999;	99US-0121825.
PR	03-MAR-1999;	99US-0123180.
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KM	Protein identification: signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter		
RW	termination sequence.		
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CS	Arabidopsis thaliana.		
XX			
PM	EPI033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PE	25-FEB-2000; 2000EP-0301439.		
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GenCore version 4.5
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OM protein - protein search, using sw model

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(without alignments)
787.234 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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11	1145.5	74.0	304	5	O25129 halocynthia
12	1125.5	72.8	307	5	O62526 drosophila
13	1102	71.2	315	4	O9HOC2 homo sapien
14	1032	66.7	300	5	O45865 caenorhabditis
15	1029	66.5	313	5	P91410 caenorhabditis
16	1029	66.5	313	5	O21103 caenorhabditis
17	986	63.7	300	5	O01813 caenorhabditis
18	985	63.7	309	5	O97470 dictyostelium
19	983	63.5	300	5	O17407 caenorhabditis

Result No.	Score	Query Match	Length	ID	Description
20	950.5	61.4	318	5	O9BU36 toxoplasma
21	949.5	61.4	307	8	O9XM22 ascaris suu
22	939	60.7	301	5	O25692 plasmodium
23	938	60.6	301	5	O26006 plasmodium
24	819	52.9	170	6	O9X569 sus scrofa
25	778	50.3	305	3	O9P8M1 yarrowia il
26	759	49.1	326	5	P91270 caenorhabditis
27	755	48.8	303	3	O74260 candida par
28	753.5	48.7	385	10	O9FY52 arabidopsis
29	753	48.7	317	5	O9N647 leishmania
30	752	48.6	307	5	O76286 trypanosoma
31	750	48.5	386	5	P93767 lycopersico
32	749.5	48.4	306	5	O18683 caenorhabditis
33	747	48.3	388	10	O49875 lupinus alb
34	746	48.2	306	3	P78754 schizosacch
35	746	48.2	306	3	O49447 arabidopsis
36	745	48.2	307	5	O26697 trypanosoma
37	740	47.8	331	10	O41628 tritlicum tu
38	721.5	46.6	305	3	O9P876 pichia jadl
39	718.5	46.4	305	3	O9P875 pichia jadl
40	690.5	44.6	330	10	O9FM86 arabidopsis
41	665.5	43.0	298	5	O21809 caenorhabditis
42	656.5	42.4	262	10	O9AVT6 picea abies
43	521.5	33.7	327	10	O9LF44 arabidopsis
44	509.5	32.9	162	5	O26130 plasmodium
45	447.5	28.9	158	5	O76467 heterodera

ALIGNMENTS

RESULT 1
ID O9PRH1 PRELIMINARY; PRT; 298 AA.
AC O9PRH1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxId=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RT Mol. Biol. Evol. 15:1612-1619(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008463; BAA36513.1; -;
DR EMBL: AB008456; BAA36506.1; -;
DR EMBL: AB008461; BAA36511.1; -;
DR EMBL: AB008462; BAA36512.1; -;
DR InterPro: IPR001993; MitoCh_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PRINTS: PRO0784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 93.5%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 1.2e-121;
Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
QY 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
Db 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180
QY 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
Db 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
QY 241 OSGRKGTDIMYGTLDCKRKIRADGSKAFKFGANSNVLRGMGAFVLYLDEIKKY 297
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGANSNVLRGMGAFVLYLDEIKKY 297

```

RESULT 2

```

Q9PRH2 PRELIMINARY: PRT: 298 AA.
ID 09PRH2:
AC Q9PRH2:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
RN NCBI_TaxID=8410;
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008460; BAA36510.1; -.
DR EMBL: AB008458; BAA36508.1; -.
DR EMBL: AB008459; BAA36509.1; -.
DR InterPro: IPR001993; Mitoch.carrier.
DR InterPro: IPR002067; Mit.carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr: 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH.CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 33082 MW; B0E225E867599A06 CRC64;

```

```

Query Match          93.3%; Score 1443; DB 13; Length 298;
Best Local Similarity 91.6%; Pred. No. 2,3e-121;
Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
QY 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
Db 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180

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QY 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
Db 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
QY 241 OSGRKGTDIMYGTLDCKRKIRADGSKAFKFGANSNVLRGMGAFVLYLDEIKKY 297
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGANSNVLRGMGAFVLYLDEIKKY 297

```

RESULT 3

```

Q9YIC4 PRELIMINARY: PRT: 298 AA.
ID 09YIC4:
AC Q9YIC4:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DE 01-JUN-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
RN NCBI_TaxID=8410;
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC EMBL: AB008457; BAA36507.1; -.
DR InterPro: IPR001993; Mitoch.carrier.
DR InterPro: IPR002067; Mit.carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr: 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH.CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 33068 MW; 15B270ED37099A00 CRC64;

```

```

Query Match          93.0%; Score 1439; DB 13; Length 298;
Best Local Similarity 91.2%; Pred. No. 5,2e-121;
Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

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```

QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKQTADKQYGIIDCVYR 60
QY 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
Db 61 IRKEDEVSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYKSDGKIGLYOGFNVS 180
QY 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
Db 181 VOGIIIRAAFGIYDTAKGMLPDPKRNTHIFISWMIAGTAVAGFASYPEDTVRRMM 240
QY 241 OSGRKGTDIMYGTLDCKRKIRADGSKAFKFGANSNVLRGMGAFVLYLDEIKKY 297
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGANSNVLRGMGAFVLYLDEIKKY 297

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RESULT 4
Q919M9 PRELIMINARY: PRT: 298 AA.
ID Q919M9

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RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -I- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BAA23777.1; -.
DR InterPro: IPR001993; Mitoch_carrter.
DR InterPro: IPR002067; Mlt_carrter.
DR Pfam: PF00153; mltc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SO SEQUENCE 298 AA; 32901 MW; CAEA32C8B164AD78 CRC64; .

Query Match 92.0%; Score 1423; DB 6; Length 298;
Best Local Similarity 89.9%; Pred. No. 1,4e-119;
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSFAKDFLFGAGVAAASIKTVAPRIERKLLLYQVHNSKQITADKQYKGIIDCVVR 60
   1:|||||
Dh 1 MSDQALSLFKDFLFGAGVAAASIKTVAPRIERKLLLYQVHNSKQISAKQYKGIIDCVVR 60
   1:|||||

QY 61 IPKEDVLSFMWGNLANVIRYFPTQALNFAEKDKYKQIFLGSVDKRTQFWRYPAGNLSAG 120
   1:|||||
Dh 61 IPKEGGLSFWRGNLANVIRYFPTQALNFAEKDKYKQIFLGSVDHKKQFWRYFAGNLSAG 120
   1:|||||

QY 121 GAAGATSLCFYVYPIDFATRIAADVGKGAKEFEFGGLDCLVYIKYKSGIINGLYGQFNVS 180
   1:|||||
Dh 121 GAAGATSLCFYVYPIDFATRIAADVGKGAKEFEFGGLDCLTKRIFKSDGLRGILYQGFNVS 180
   1:|||||

```

```

Db      181 VGGIIITVAAATGCVDTAKGMLPLDPKKNHIIIVSMIAIQTVTAAGLVSPDPTVARRRMM 240
Qy      241 OSGRKGTDIMYTGTLDCWRKIARDEGKAFFKGAMSNVLRGMGAFVLYLDEIKKY 297
        |||||T|||||T|||||T|||||T|||||T|||||T|||||T|||||T|||||T|||||
Db      241 OSGRKGADIMYTGTVDCKWKIATADEGAFAFKGAMSNVLRLGMGAFVLYLDEIKKY 297

RESULT    6
ID         062164          PRELIMINARY;             PRT;       298 AA.
AC         062164;
DT         01-NOV-1996 (TREMBLrel. 01, Created)
DT         01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT         01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE         ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR
DE         TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE
DE         TRANSLOCATOR), MEMBER 4).
CN         SLG25A4 OR MANC1 OR ANM1.
OS         Mus musculus (Mouse).
OC         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX         NCBI_TaxID=10090;
RN         [1]
RP         SEQUENCE FROM N.A.
RC         STRAIN=BALB/C; TISSUE=MUSCLE;
RA         Laplace C., Costet P.;
RL         Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
RN         [2]
RP         SEQUENCE FROM N.A.
RC         Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RA         "Expression and sequence analysis of the mouse adenine nucleotide
RT         translocase 1 and 2 genes.";
RL         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN         [3]
RP         SEQUENCE FROM N.A.
RC         Strausberg R.;
RA         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC         -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
           INNER MEMBRANE (BY SIMILARITY).
CC         -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR         EMBL: J74510; CAA52616.1; -.

```


DE HYPOTHEETICAL 35.0 KDA PROTEIN.
GN DKF2P434N1235.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AL336857; CAB66791.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00153; mltc_carrt; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 1.
KW Hypothetical protein; Inner membrane; Mitochondrion; Transmembrane;
KW Transport. 315 AA; 35022 MW; 9ACE26062CC9675 CRC64;
SQ SEQUENCE

Query Match	71.28;	Score 1102;	DB 4;	Length 315;
Best Local Similarly	71.78;	Pred. No. 9.2e-91;		
Matches 210;	Conservative 34;	Mismatches 47;	Indels 2;	Gaps 1;

[illegible]

RESULT 14

ID 045865 PRELIMINARY; PRT; 300 AA.

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

GN T27E9.1.

OC Eukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida: Rhabditoidea:

NCBI TaxID=6239:

RP	SEQUENCE FROM N.A.
KN	[11]

KA
LLOYD C.;
Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases

RN [2]
PB
SEQUENCE FROM N A

W11500 B A15000000 B Addon
MEDLINE=94150718; PubMed=7906398

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Croxall M., Dear G., Dunn S., Fawcett A., Fullard J.,

RA Gardner A., Green P., Haxkins T., Hillier L., Jier M., Johnston L.
RA Jones M., Kershaw J., Kingston J., Laister N., Lattelle P.,
RA Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkseen
RA Smalodon N., Smith A., Sonnhemmer E., Staden R., Sulston J.,
RA Thierly-Wieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spoat J., Wohlfman P.,
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
RT elegans* *;
RL Nature 368:32-38(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: Z82059; CAB04874.1; -
DR InterPro: IPR001993; Mitoch.cARRIER.
DR InterPro: IPR002067; Mlt.cARRIER.
DR Pfam: PF00153; mito.carrt. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
KW SEQUENCE 300 AA; 33044 MW; BE50F7DDA5933C6E CRC64;

Query Match	66.7%	Score 1032	DB 5	Length 300
Best Local Similarity	69.8%	Pred. No. 1.6e-84		
Matches 203	34	Mismatches 50	Indels 4	Gaps 3

[illegible]

RESULT 15

ID P91410 PRELIMINARY; PRT; 313 AA.

DT 01-MAY-1997 (TREMBLrel. 03, Created

DT 01-JUN-2001 (Tremblay, 17, Last annotation update)

GN T01B11.4.

03 Eukaryot

NCBI TaxID=62339:

BP
KN
[]
SEQUENCE FROM N. A.

RX MEDLINE=94150718: PubMed=7906398

RA Wilson R., Anderson K., Baynes C., Belks M.,
PA Bonfield J, Burton I, Connell M, Cooney T, Cooper J, Coulson A

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green D., Harding E., Hillier I., Jones M., Johnston I.

RA Jones M., Kershaw J., Kirsten J., Laister N., Latrelle P.,
 RA Richards T., Lloyd C., Mervin J., Mervin D., O'Callaghan W.

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Steilyes L.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; 080931; AAB38001.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carf; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 313 AA: 34356 MW: CF07C473A719CCB6 CRC64;

Query Match 66.5%; Score 1029; DB 5; Length 313;
 Best Local Similarity 70.8%; Pred. No. 3.2e-84;

Matches 206; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

OY 8 FAKDELAGVAAAIKSTAVAPIERVKLLQVQHASQKITADKQYKGIIDCVVRIPKEDEV 67
 DB 25 FLIDLASGCTAAAVSKTAVAPIERYKLLQVODASLTIAADKRYKGIIDVLRVPREQGY 84
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFWRYPAGNLAGGAAGATS 127
 DB 85 AALMRGNLANVIRYPTQALNFAFKDYKNIFQGLDKRKDFWKFPAGNLAGGAAGATS 144
 OY 128 LCFVYPLDFARTRLADYVKGAGEREFRGLGDLVYKYSKGIGLYOGFNYSVOGIITY 187
 DB 145 LCFVYPLDFARTRLADYVKAN-EREFKLADCLVYKIAKSDGPIGLYRGFFYSVOGIITY 203
 OY 188 RAAVGIYDTAKGML-PDEKNTNIVISWMIQOTVAVAGLTSYPEDTVRRMMQSGRGK 246
 DB 204 RAAVGMEDTAKMFTADGKLNFFAAMAIQVVTGSGILSYPMDTVRRMMQSGRK- 262
 OY 247 TDIMYTGTLDCARKIARDEGKAFKFGAMSNTLRMGCAFVLIVDEIKKY 297
 DB 263 -DVLKNTLDCAVKIKNEGMSAMFRGALSNVFRGTGALVLAIDYDEIQKF 312

Search completed: February 13, 2002, 09:34:15
 Job time: 172 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:34:42 ; Search time 22.53 Seconds

(Without alignments)
484,959 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547
Sequence: 1 MTDALSPFAKDFLAGVAA.....LRMGAFVLYLDEIKKKT 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	99.4	298	1	ADT2_HUMAN
2	1525	98.6	298	1	ADT2_RAT
3	1519	98.2	298	1	ADT2_MOUSE
4	1458	94.2	298	1	ADT3_BOVIN
5	1454	94.0	298	1	ADT3_HUMAN
6	1417	91.6	298	1	ADT1_RAT
7	1414	91.4	297	1	ADT1_BOVIN
8	1413	91.3	298	1	ADT1_HUMAN
9	1411	91.2	298	1	ADT1_MOUSE
10	1218.5	78.8	297	1	ADT1_DROME
11	1190	76.9	301	1	ADT1_ANOXA
12	968	62.6	339	1	ADT1_CHLKE
13	771	49.8	326	1	ADT1_GOSHI
14	770	49.8	322	1	ADT1_SCHPO
15	765	49.5	308	1	ADT3_CHLRE
16	761.5	49.2	307	1	ADT3_YEAST
17	759	49.1	387	1	ADT1_MAIZE
18	757	48.9	313	1	ADT1_NEUCR
19	753	48.7	387	1	ADT1_MAIZE
20	752.5	48.6	318	1	ADT2_YEAST
21	752	48.6	386	1	ADT1_SOLITU
22	750	48.5	382	1	ADT1_ORYSA
23	749.5	48.4	305	1	ADT1_KILUA
24	747.5	48.3	381	1	ADT1_ARATH
25	745.5	48.2	385	1	ADT1_ARATH
26	744	48.1	331	1	ADT2_WHEAT
27	741.5	47.9	331	1	ADT2_SOLITU
28	737	47.6	331	1	ADT2_WHEAT
29	728	47.1	309	1	ADT1_YEAST
30	302	19.5	587	1	CMC3_CAEEL
31	302	19.5	587	1	CMC3_CAEEL
32	285	18.4	350	1	GDC_BOVIN
33	284	18.4	307	1	YOTL_YEAST

34	278	18.0	322	1	BMC2_MOUSE
35	276.5	17.9	322	1	GDC_RAT
36	276.5	17.9	702	1	CMC1_CAEEL
37	276	17.8	678	1	BMC2_HUMAN
38	274	17.7	325	1	BMC2_HUMAN
39	265.5	17.2	332	1	GDC_HUMAN
40	261.5	16.9	675	1	CMC2_HUMAN
41	249.5	16.1	326	1	YR08_SCHPO
42	249	16.1	324	1	PRT_YEAST
43	249	16.1	676	1	CMC2_MOUSE
44	249	16.1	695	1	CMC1_DROME
45	247	16.0	312	1	UCP3_HUMAN

ALIGNMENTS

RESULT 1	ADT2_HUMAN	STANDARD	PRT: 298 AA.
AC	P05141: 043350;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	01-OCT-1994 (Rel. 30, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	ADP-ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)		
DE	(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).		
CN	SLC25A5 OR ANT2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=90375457; PubMed=2168878;		
RA	Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;		
RT	"The human fibroblast adenine nucleotide translocator gene. Molecular cloning and sequence."		
RL	J. Biol. Chem. 265:16060-16063(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=87166056; PubMed=3031073;		
RA	Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,		
RT	Baserga R.;		
RT	"Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated."		
RL	J. Biol. Chem. 262:4355-4358(1987).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Chen C.-N., Su Y., Baybayan P., Siruno A., Nagaraja R.,		
RA	Mazarella R.A., Schlesinger D., Chen E.Y.;		
RT	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Becker M., Graves T., Ozersky P.;		
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RP	SEQUENCE OF 47-298 FROM N.A.		
RC	TISSUE=Liver;		
RX	MEDLINE=88124845; PubMed=2829183;		
RA	Houldsworth J., Altardi G.;		
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver."		
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).		
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE		
CC	MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- SUBUNIT: HOMODIMER.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE.		
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
CC	-----		
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CC -----
 DR EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: J78810; AAA39266.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR MIM: 300150; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 FT SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best Local Similarity 99.3%; Pred. No. 9.5e-130;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDALSFADKPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKIIDCVRR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKIIDCVRR 60
 QY 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLAGS 120
 DB 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGLYOGFNVS 180
 QY 181 VGGIITRYRAAYFGIYDTAGMLDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 DB 181 VGGIITRYRAAYFGIYDTAGMLDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 QY 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAGVVLVLYDEIKKYYT 298
 DB 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAGVVLVLYDEIKKYYT 298

RESULT 2
 ADP2_RAT
 ID ADP2_RAT STANDARD: PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP: ATP CARRIER PROTEIN, F1BROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADENINE NUCLEOTIDE TRANSLATOR 2) (ANT 2).

GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RL encoding rat mitochondrial adenine nucleotide translocator";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1 SUBUNIT: HOMODIMER.
 CC -1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1 TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).

CC EMBL: D12771; BAA02238.1; -
 CC InterPro: IPR002067; Mlt_carrier.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr; 3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PRINTS: PR00927; ADPTRNSLCASE.
 CC PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA; 32901 MW; 6A59204B987EFEE35 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 1.1e-128;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDALSFADKPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKIIDCVRR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKIIDCVRR 60
 QY 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLAGS 120
 DB 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGLYOGFNVS 180
 QY 181 VGGIITRYRAAYFGIYDTAGMLDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 DB 181 VGGIITRYRAAYFGIYDTAGMLDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 QY 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAGVVLVLYDEIKKYYT 298


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DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match
Best Local Similarity 94.2%; Score 1458; DB 1: Length 298;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGGVAIAISKTAVPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
DB 1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVQHASKQIADKQYKGIIDCVR 60
QY 61 IPREQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 IPREQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKRTPLADVGKAGAREFRGIGDCLVYIYSDGIKGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDPAKRTPLADVGKSGSERFRGIGDCLVYITKSDGIRGLYOGFNVS 180
QY 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTIVISMIAQVTAAGVLSYFEDTVRRRMM 240
DB 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTIVISMIAQVTAAGVLSYFEDTVRRRMM 240
QY 241 QSGRKGTIDIMYTGTLDCWKRIARDEGKAFKAGMSNVLRGMGAFVLYLDEIKK 296
DB 241 QSGRKGDIMYTGTLDCWKRIARDEGKAFKAGMSNVLRGMGAFVLYLDEIKK 296

RESULT 5
ADP3_HUMAN STANDARD; PRT; 298 AA.
ID ADP3_HUMAN STANDARD; PRT; 298 AA.
AC P12236;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).
GN SLG25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RP [2]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).

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CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: J03592; AAA36750.1; -.
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR MIM: 300151; -.
DR MIM: 403000; -.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 2).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match
Best Local Similarity 94.0%; Score 1454; DB 1: Length 298;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGGVAIAISKTAVPIERVKLLQVQHASKQITADKQYKGIIDCVR 60
DB 1 MTEQAISFAKDFLAGGIAAISTAVAPIERVKLLQVQHASKQIADKQYKGIIDCVR 60
QY 61 IPREQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
DB 61 IPREQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKRTPLADVGKAGAREFRGIGDCLVYIYSDGIKGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDPAKRTPLADVGKSGSERFRGIGDCLVYITKSDGIRGLYOGFNVS 180
QY 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTIVISMIAQVTAAGVLSYFEDTVRRRMM 240
DB 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTIVISMIAQVTAAGVLSYFEDTVRRRMM 240
QY 241 QSGRKGTIDIMYTGTLDCWKRIARDEGKAFKAGMSNVLRGMGAFVLYLDEIKK 296
DB 241 QSGRKGDIMYTGTLDCWKRIARDEGKAFKAGMSNVLRGMGAFVLYLDEIKK 296

RESULT 6
ADP1_RAT STANDARD; PRT; 298 AA.
ID ADP1_RAT STANDARD; PRT; 298 AA.
AC O05962;
DT 01-FEB-1994 (Rel. 28, Last sequence update)

```

20-AUG-2001 (Rel. 40, last annotation update)
 DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
 TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY, AND WISTAR; TISSUE=Heart, and Liver;
 RA MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X61667; CA43842.1; -
 DR EMBL: D12770; BAA0237.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MW; 66704EFF78C6BC320 CRC64;
 Query Match 91.6%; Score 1417; DB 1; Length 298;
 Best local Similarity 89.6%; Pred. No. 4.6e-119;
 Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

DB 181 VGGIIIRAAVFGIYDTAKMLDPPKNTHTIVISWIAQTAVAGLTSYFPDVRRRMM 240
 ||||||||||||||||||||||||||| : : : ||||||| |||||||||||
 QY 241 QSRKRGTDIWTGTLDCKRKRIARDEGKAFFKGAWSNVLRGKGAPVLYDEIKRY 297
 ||||| ||||||| : : : ||||||| : : : ||||||| : : : |||||||
 DB 241 QSRKRGADIWTGTDCWKRRIARDEGKAFFKGAWSNVLRGKGAPVLYDEIKRY 297
 ||||||||||||||||||||||||||| : : : ||||||| |||||||||||
 RESULT 7
 ID ADT1_BOVIN STANDARD; PRT; 297 AA.
 AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 20-AUG-2001 (Rel. 40, last annotation update)
 DE ADP/ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
 DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=89229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT Two bovine genes for mitochondrial ADP/ATP translocase expressed
 RT differences in various tissues.";
 RL Biochemistry 28:866-873(1989).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=82188267; PubMed=7076130;
 RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
 RT mitochondria.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
 RN [3]
 RP SEQUENCE OF 207-297 FROM N.A.
 RX MEDLINE=86295775; PubMed=3017341;
 RA Rasmussen U.B., Wohlrab H.;
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
 RT an unusually short 3'-noncoding sequence.";
 RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M13783; AAA30363.1; -
 DR EMBL: M24102; AAA30768.1; -
 DR PIR: A03181; XWBO
 DR PIR: A24822; A24822.
 DR PIR: A43646; A43646.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Methylation.

```

FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA: 32836 MW: A582D3CA4A0AE48 CRC64:

Query Match 91.4%: Score 1414: DB 1: Length 297:
Best Local Similarity 89.9%: Pred. No. 8.6e-119:
Matches 265: Conservative 16: Mismatches 14: Indels 0: Gaps 0:

OY 2 TDAALSFADPLAGVAAAIKSTAVAPIERVKLLQVHASKQITADKQYGIIDCVRI 61
DB 1 SQOALSFKLDFLAGVAAAIKSTAVAPIERVKLLQVHASKQISAEKQYGIIDCVRI 60
OY 62 PREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 121
DB 61 PREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
OY 122 AAGATSLCFVYPLDFARFRLADVGKAGAREPFGDCLVYIKYSGIKLYGPFNVSV 181
DB 121 AAGATSLCFVYPLDFARFRLADVGKAGAREPFGDCLVYIKYSGIKLYGPFNVSV 180
OY 182 OGIIIRAAVFGIYDTANGMLDPKRNTHLVISMIAQVTAVAGLTSYFEDTVRRMMQ 241
DB 181 OGIIIRAAVFGIYDTANGMLDPKRNTHLVISMIAQVTAVAGLTSYFEDTVRRMMQ 240
OY 242 SGRKGTDMYTTGLDCKRIARDEGKAFKFGKANSVNLGMCAGAYLVLYDEIKRY 297
DB 241 SGRKGTDMYTTGLDCKRIARDEGKAFKFGKANSVNLGMCAGAYLVLYDEIKRY 296

RESULT 8
ADT1_HUMAN STANDARD: PRT: 298 AA.
ID ADT1_HUMAN PRT: 298 AA.
AC P12235:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP-ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodges J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed."
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

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RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02966; AAN6123.1; -
DR EMBL: J03593; AAN36751.1; -
DR EMBL: J04982; AAN51736.1; -
DR PIR: A28116; A28116.
DR PIR: A39891; A39891.
DR PIR: S03893; S03893.
DR PIR: A44778; A44778.
DR MIM: 103220; -
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLOCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 16 16 G -> A (IN REF. 3).
FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
FT CONFLICT 227 227 V -> L (IN REF. 3).
SQ SEQUENCE 298 AA: 33064 MW: 59F0DFAEC4E7CFBB CRC64:

Query Match 91.3%: Score 1413: DB 1: Length 298:
Best Local Similarity 89.2%: Pred. No. 1.1e-118:
Matches 265: Conservative 16: Mismatches 16: Indels 0: Gaps 0:

OY 1 MTDALSFADPLAGVAAAIKSTAVAPIERVKLLQVHASKQITADKQYGIIDCVRI 60
DB 1 MTDHMSFLKDLFAGVAAAIKSTAVAPIERVKLLQVHASKQISAEKQYGIIDCVRI 60
OY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARFRLADVGKAGAREPFGDCLVYIKYSGIKLYGPFNVSV 180

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Db 121 GAAGATSLCFVYPLDFAFRLADVGKAAQREFHGLDCLIKIFKSDGLRGHYOGFNVS 180
QY 181 VGGIITIRAAVFCIYDTAKMLDPKNTHTIVISMIAQOTAVAGLTSYFEDTVRRRMM 240
Db 181 VGGIITIRAAVFCIYDTAKMLDPKNTHTIVISMIAQOTAVAGLTSYFEDTVRRRMM 240
QY 241 QSGRKGTIDIMYTGLDQWRKRIARDEGKAFKFGAMSVNLGKMGAFVLYDEIRKY 297
Db 241 QSGRKGTIDIMYTGLDQWRKRIARDEGKAFKFGAMSVNLGKMGAFVLYDEIRKY 297

RESULT 9
ADT1_MOUSE STANDARD: PRT: 298 AA.
AC P48962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. genome 7:25-30(1996).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27315; AAC52837.1; -
DR MGD: MG1:1353495; SLC25a4.
DR InterPro: IPR002067; MitCarrier.
DR InterPro: IPR001993; MitochCarrier.
DR Pfam: PF00153; mito-car1.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCLASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SO SEQUENCE 298 AA; 32870 MW; 32AC3B4EFCFA482 CRC64;

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Query Match 91.2%; Score 1411; DB 1; Length 298;
Best Local Similarity 89.2%; Pred. No. 1, 6e-118;

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Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MTPAALSFADKPLAGVAAALISKTAAPERVRKLLLOVGHASQIRADKQKIIICVVR 60
Db 1 MGDALSLFDPLDLAGIAAASVSTAAPERVRKLLLOVGHASQIRADKQKIIICVVR 60
QY 61 IPKEQELSFWRGNLNVIRYPTQALNFAFKDKYKQIFLGADKRTQEFRRYFAGNLASG 120
Db 61 IPKEQELSFWRGNLNVIRYPTQALNFAFKDKYKQIFLGADKRTQEFRRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAFRLADVGKAAQREFHGLDCLIKIFKSDGLRGHYOGFNVS 180
Db 121 GAAGATSLCFVYPLDFAFRLADVGKAAQREFHGLDCLIKIFKSDGLRGHYOGFNVS 180
QY 181 VGGIITIRAAVFCIYDTAKMLDPKNTHTIVISMIAQOTAVAGLTSYFEDTVRRRMM 240
Db 181 VGGIITIRAAVFCIYDTAKMLDPKNTHTIVISMIAQOTAVAGLTSYFEDTVRRRMM 240
QY 241 QSGRKGTIDIMYTGLDQWRKRIARDEGKAFKFGAMSVNLGKMGAFVLYDEIRKY 297
Db 241 QSGRKGTIDIMYTGLDQWRKRIARDEGKAFKFGAMSVNLGKMGAFVLYDEIRKY 297

RESULT 10
ADT1_DROME STANDARD: PRT: 297 AA.
AC Q26365; Q26254; P91614; Q9V270;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLOCATOR) (ANT) (STRESS SENSITIVE B PROTEIN).
GN SESB OR A/A-T OR CG16944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92389367; PubMed=1387687;
RA Louvi A., Tsililou S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT melanogaster shows a high degree of similarity with the mammalian
RT ADP/ATP translocases."
RL J. Mol. Evol. 35:44-50(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=94350065; PubMed=7520869;
RA Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
RT isolation between sibling species of Drosophila."
RL Experientia 50:749-762(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=OREGON-R;
RA Zhang Y.O., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RA Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Cherry J.M., Cavley S., Dahlike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibeagwa C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Liao P., Lei Y., Levitsky A.A., Li Y., Li Z., Liang Y., Lin X.,
 RA Lin X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J.J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclele J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Slden-Klamas I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Weiss A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Wengenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC EMBL: S43651; AAB23114.1; -;
 DR EMBL: S71762; AAB31734.3; -;
 DR EMBL: Y10618; CAA71628.1; -;
 DR EMBL: AE003484; AAF47957.1; -;
 DR Flybase: FBgn0003360; sess.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mltc_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT CONFLICT 18 19 QV -> GI (IN REF. 3 AND 4).
 FT CONFLICT 81 81 I -> Y (IN REF. 1).
 FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
 FT CONFLICT 266 266 G -> A (IN REF. 2).
 FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT CONFLICT 268 268 C -> S (IN REF. 1).
 SQ SEQUENCE 297 AA: 32880 MW: 66334.39968 PF750 CRC64:

Query Match	78.8%	Score 1218.5	DB 1	Length 297
Best Local Similarity	80.5%	Pred. No. 2.2e-101		
Matches 253	Conservative 20	Mismatches 34	Indels 3	Gaps 3

ID	ADP	ANOGA	STANDARD	PRT	301 AA
QY	5	ALSFKDEFLAGVAAAIKSTAAVPIERKLLLOVHASKOTJADQYGIIDCVIRIKE			64
Db	7	AGCFVKDRAQGVSAVSKTAAVPIERKLLLOVHASKOTJADQYGIIDCVIRIKE			66
QY	65	QEVLSFWMGNTLANVIRPEPTQALNFAFKDKYKQIFLGGVDKRTQWRYFAGNLASGGAAG			124
Db	67	QCFSSFWMGNTLANVIRPEPTQALNFAFKDKYKQIFLGGVDKRTQWRYFAGNLASGGAAG			126
QY	125	ATSLCFVYPLDFARFRLAADGKAGAEKFEKGLDCLVYKIKSDGIKGLYOGFNVVOCI			184
Db	127	ATSLCFVYPLDFARFRLAADGKAGAEKFEKGLDCLVYKIKSDGIKGLYOGFNVVOCI			185
QY	185	IIFYRAAYGIYDTAGAGLPPDKNTHIVISWMTAQQVTVFVAGTFSYEPDTVRRMMOSGR			244
Db	186	IIFYRAAYGIYDTAGAGLPPDKNTHIVISWMTAQQVTVFVAGTFSYEPDTVRRMMOSGR			244
QY	245	KGTIDMYTGTLDCWKRRIARDEGKAFKFGAMSVNLRGSGAFVLYLDEIKK			296
Db	245	KATEVIYKNTLHCWMTIAKQE-GPCFFKFGAFSNILRGSGAFVLYLDEIKK			295
RESULT	11				
ADT	ADT	ANOGA	STANDARD	PRT	301 AA
AC	Q27238				
AT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT).				
OS	Anopheles gambiae (African malaria mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;				
OC	Anopheles.				
OX	NCBI_TaxID=7165;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=G3;				
RX	MEDLINE=94348635; PubMed=8069414;				
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;				
RT	"A CDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae."				
RL	Insect Mol. Biol. 3:35-40(1994).				
CC	- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.				
CC	- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL INNER MEMBRANE.				
CC	- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
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CC					
DR	EMBL, L11618; AAB04104.1; -				
DR	EMBL, L11617; AAB04105.1; -				
DR	InterPro, IPR002067; Mlt_carrier.				
DR	InterPro, IPR001993; Mltocb_carrier.				
DR	Pfam, PF00153; mltc_carr; 3.				
DR	PRINTS: PR00926; MITOCH_CARRIER.				
DR	PRINTS: PR00927; ADPPTSLOCASE.				
KW	PROSITE, PS00215; MITOCH_CARRIER, 3.				
CC	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.				
FT	TRANSMEM 14	31	1 (POTENTIAL).		
FT	TRANSMEM 75	93	2 (POTENTIAL).		
FT	TRANSMEM 119	136	3 (POTENTIAL).		
FT	TRANSMEM 178	197	4 (POTENTIAL).		


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DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 1 76 ADP/ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 386 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 312 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42093 MW; A05F76C73FECDEE6 CRC64;

Query Match 49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. No. 2.2e-61;
Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;

OY 7 SFAPDLGAGVAAAIKSTVAPIERVKLLQVQ-HASKQITADKQYGIIDCVRIPEQ 65
DP 85 SFAPDLGAGVAAAIKSTVAPIERVKLLQVQ-HASKQITADKQYGIIDCVRIPEQ 144
OY 66 EVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASGAGA 125
DB 145 GFGSLMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASGAGA 203
OY 126 TSLSFVYPPDFAFRTLAAD--VGKAGAREFRGLGDCLVKIKYKSDGKIGYGFENVYOG 183
DB 204 SLSLFVYSLDYARTRLANDAKAKKGGEROFNGLVYRKRTLSKDSIAGLRKFNFISCVG 263
OY 184 IIRAYRFGIYDTAK-----GMLPDPKNTNIVISMIAQVTAAGLTSYPTDVRRRM 238
DB 264 IIVRYRLYFGMDSLKPVLLTSGMQDSFFASFYLGWLI---TNGAALASYPIDTVRRRM 319
OY 239 MMSGKRGTDIMWTGLDCKRKIARDEGKAFKFGKMSVNLKMGAFVLYLVDEL---- 294
DB 320 MMTSGKA---VYKSSLDLAFSOLKNEGKSLFKGAGSNILRAIAGVLAGYDKLQILY 376
OY 295 --KKY 297
DB 377 FGKXY 381

RESULT 14
ADT_SCHPO STANDARD: PRT: 322 AA.
AC 009188:
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLCATOR) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
RT carrier of Schizosaccharomyces pombe by functional complementation in
RT Saccharomyces cerevisiae.";
RL Gene 171:113-117(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.;

```

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RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -! SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -! DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z49974; CAA90275.1; -
DR EMBL: AL023634; CAA19176.1; -.
DR HSP: P04002; IATF.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 1 (POTENTIAL).
FT TRANSMEM 93 111 2 (POTENTIAL).
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 222 242 5 (POTENTIAL).
FT TRANSMEM 289 309 6 (POTENTIAL).
SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;

Query Match 49.8%; Score 770; DB 1; Length 322;
Best Local Similarity 53.6%; Pred. No. 2.2e-61;
Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;

OY 7 SFAPDLGAGVAAAIKSTVAPIERVKLLQVQ-HASKQITADKQYGIIDCVRIPEQ 63
DB 26 TFFDFPMGGSAAVSKTAAPIERVKLLQVQ--DEMIRARLSHRKIGIECKRRTAA 83
OY 64 EGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASGAGA 123
DB 84 EGVLSFMRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLASGAGA 142
OY 124 GATSLCFVYPPDFAFRTLAAD--GKAGAREFRGLGDCLVKIKYKSDGKIGYGFENVY 181
DB 143 GASLSLFVYSLDYARTRLANDAKAKKGGEROFNGLVYRKRTLSKDSIAGLRKFNFISCV 202
OY 182 OGIIIRAYRFGIYDTAK--MLPDPKNTNIVISMIAQVTAAGLTSYPTDVRRRM 240
DB 203 VGIIVRYRGLYFGMDSLKPVLLTSGMQDSFFASFYLGWLI---TNGAALASYPIDTVRRRM 262
OY 241 OSGRKGTDMWTGLDCKRKIARDEGKAFKFGKMSVNLKMGAFVLYLVDEL---- 295
DB 263 TSGEA---VKYSSFEQGLIILAKEGARSFPGAGANILRGVAGVLSIYDQV 314

RESULT 15
ADT_CHLRE STANDARD: PRT: 308 AA.
AC P27080:
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 01-OCT-1994 (rel. 30, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLCATOR) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

```

Search completed: February 13, 2002, 09:34:43
Job time: 200 sec

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OC Chlamydomonadaceae: Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FUDA4-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP
  translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
  MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X65194; CAA46311.1; -.
DR PIR: S30259; S30259.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PRINTS: PRO0927; ADPTENSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KM Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CFDE72B7A53F CRC64;

Query Match 49.5%; Score 765; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 5,8e-61;
Matches 159; Conservative 49; Mismatches 78; Indels 16; Gaps 6;

OY 7 SFAPKDLAGVAAAIKSTAVAPIERVKLLIQV-HASKQITADKQYGIIDCVIRPKEQ 65
   :| | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 NFVVDFLAGLSAAVSKTAAPIERVKLLIQNDDEMIKQGRSLAPYKGIQCEFEVRTVREE 66

OY 66 EVLSFWMGNLANTRYPPQALNPAFKDKYKOTFLGVDKRTQFWRYPAGNLASGAGA 125
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 GFGSLMRGNTANVIRIFPTQALNPAFKDKTRMF--GFNNDKEYKWFAGNMASSGAGA 124

OY 126 TSLCFVYPLDFAFRLAAD--VGKACAREFERGLGDLVKIKYSDGIKGLYQGFNVSQ 182
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 125 VSLSEFVSLDYARTLANDAKSAKKGGRQFNGLVYRRTIASDGIAGLYRGFNISCV 184

OY 183 GIIIRAAVFGIYDTANG-MLPDPKNTIYISMMIAQTVAVAGLTSYPPDYVRRMMQ 241
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 185 GIIVYRGLYFGMDLKLPLVGLPFLANNFLAFLGIGITIGAGLASYPIDTIRRRMMT 244

OY 242 SGRGTDIMTGTLDGWRKLTARDEGKAFKGAWSNVLRGMGAFFVLVYDEI-----K 295
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 245 S---GSAVKYNSFRHCQEIYKNEGMSLFRKAGANILRAVAGVLAGYDQLCVIILGK 301

OY 296 KY 297
   ||
Db 302 KY 303
```


GenCore version 4.5
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OW protein - protein search, using sw model

Run on: February 13, 2002, 09:32:07 ; Search time 34.78 Seconds

(without alignments)
652.674 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDALSPAKDFLAGVAAA.....LRGMGARFVLVDEIRKVT 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	1 A29132	ADP, ATP carrier pr
2	1479	95.6	298	2 S31814	ADP, ATP carrier pr
3	1458	94.2	298	2 B43646	ADP, ATP carrier pr
4	1454	94.0	298	1 S03894	ADP, ATP carrier pr
5	1419	91.7	298	1 XWBO	ADP, ATP carrier pr
6	1417	91.6	298	2 S37210	ADP, ATP carrier pr
7	1417	91.6	298	2 S37210	adenine nucleotide
8	1413	91.3	298	1 A44778	ADP, ATP carrier pr
9	1170	73.6	301	1 S31935	ADP, ATP carrier pr
10	1032	66.7	300	2 T23571	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T25850	hypothetical prote
13	986	63.7	300	2 T15206	hypothetical prote
14	968	62.6	339	2 A41677	ADP, ATP carrier pr
15	938	60.6	301	2 S51132	ADP, ATP carrier pr
16	771	49.8	386	2 T09709	ADP, ATP carrier pr
17	770	49.8	322	2 T40526	ADP, ATP carrier pr
18	765	49.5	308	2 S30259	ADP, ATP carrier pr
19	761.5	49.2	307	2 A36582	ADP, ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	387	2 S14876	ADP, ATP carrier pr
22	757	48.9	313	1 XWMC	ADP, ATP carrier pr
23	754	48.7	386	2 S17917	ADP, ATP carrier pr
24	753	48.7	387	2 S16568	ADP, ATP carrier pr
25	752.5	48.6	318	1 A21974	ADP, ATP carrier pr
26	752	48.6	386	2 S21974	ADP, ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP, ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP, ATP carrier pr

30	746	48.2	379	2 T04608	ADP, ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP, ATP carrier pr
32	745	48.2	382	2 S33630	ADP, ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP, ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP, ATP carrier pr
35	728	47.1	309	2 A24849	ADP, ATP carrier pr
36	665.5	43.0	298	2 T24029	hypothetical prote
37	521.5	33.7	327	2 T51577	ADP, ATP translocas
38	388	25.1	325	2 T04273	hypothetical prote
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	mitochondrial solu
42	350	22.6	475	2 T50686	peroxisomal Ca-dep
43	340	22.0	358	2 T45934	hypothetical prote
44	334	21.6	348	2 D84798	probable mitochond
45	322.5	20.8	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1

A29132
ADP, ATP carrier protein T2 - human
N:Alternate names: mitochondrial ADP, ATP translocase 2
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A29132; C28116
J:Ballini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
R: Biol. Chem. 267, 4355-4359, 1997
A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu
A:Reference number: A29132; MUID:87166056
A:Accession: A29132
A:Molecule type: mRNA
A:Residues: 1-298 <BAT>
A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
R:Houldsworth, J.; Atcardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:8812845
A:Accession: C28116
A:Molecule type: mRNA
A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
A:Experimental source: clone PHAT3
C:Genetics:
A:Gene: GDB:ANT2; T3; 2P1
A:Cross-references: GDB:125190; OMIM:300150
A:Map position: Xq13-Xq26
A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1547; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 2e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAISKTAFAVPIERVKLLLOVQHSKQITADKQKGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAAISKTAFAVPIERVKLLLOVQHSKQITADKQKGIIDCVR 60
QY 61 IPKQEVLSFMKGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
DB 61 IPKQEVLSFMKGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
QY 121 GAAGATSLCEFYVPLDFAFRTRLADVYKAGAEERERGLGDCLVKTKYKSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCEFYVPLDFAFRTRLADVYKAGAEERERGLGDCLVKTKYKSDGKIGLYOGFNVS 180

Oy	181	VOGIIITVAAAFEGYIDTAKKGM	PPDKNNHIYISWIAQTVAVAGLSTYPPDTVRRMM	240
Db	181	VOGIIITVAAAFGCIYDTAKKGM	PPDKNNHIYISWIAQTVAVAGLSTYPPDTVRRMM	240
Oy	241	OSGRKGTDMYTGTLDDCKRIAR	DEGKAFFKGAANSVLRGCGAFVLYLDEIKYT	298
Db	241	OSGRKGTDMYTGTLDDCKRIAR	DEGKAFFKGAANSVLRGCGAFVLYLDEIKYT	298
RESULT	2			
S31814		ADP, ATP carrier protein T2 - mouse		
N:	Alternate names:	adenine nucleotide translocase		
C:	Species:	Mus musculus (house mouse)		
C:	Date:	06-Jan-1995 #sequence_revision		
C:	Accession:	S31814		
R:	Costet, P.; Laplace, C.			
	submitted to the EMBL Data Library, January 1993			
A:	Reference number:	S31814		
A:	Accession:	S31814		
A:	Status:	preliminary		
A:	Molecule type:	mRNA		
A:	Residues:	1-298 <COS>		
C:	Cross-references:	EMBL:X70847		
C:	Superfamily:	ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology <ACPI>		
C:	Keywords:	duplication; transmembrane protein		
E:	110-202/Domain:	ADP, ATP carrier protein repeat homology <ACPI>		
E:	110-202/Domain:	ADP, ATP carrier protein repeat homology <ACPI>		
E:	207-298/Domain:	ADP, ATP carrier protein repeat homology <ACPI>		

Query Match	95.68;	Score 1479;	DB 2;	length 298;
Best Local Similarity	95.68;	Pred. No. 2.1e-123;		
Matches 285; Conservative	4;	Mismatches 9;	Indels 0;	Gaps 0;

Oy	1	MTDALSPAKOFLAGVAAAIKSTVAAIERKLLLOYOHSAKOTAPKOYKGIIDCVR	60
Oy	1	MTDALSPAKOFLAGVAAAIKSTVAAIERKLLLOYOHSAKOTAPKOYKGIIDCVR	60
Db	1	MTDAVSPAKPDLACGVAAAIKSTVAAPLERKLLMOYQTNDRITTAADKOYKGIIDCVR	60
Oy	61	IPKBEVLSFMRGNLANIYRIFPTOALNFAFEDKTKOJIFLGVDKRTOPMRFAGNLASG	120
Db	61	IPKEGVLSFMRGNLANIYRIFPTOALNFAFEDKTKOJIFLGVDKRTOPMRFAGNLASG	120
Oy	121	GAAGATSLCFVYPLDFEARTRLAADVGKAAKEPREFGLDCLVIKYSOGIKGLYOGFNVS	180
Db	121	GAAGATSLCFVYPLDFEARTRLAADVGKAAKEPREFGLDCLVIKYSOGIKGLYOGFNVS	180
Oy	181	VOGIITIRAAVYFGIYDTAKGMLPDEKNHIVISWMIACOTVTAVAGLTYSPEDDVRRMM	240
Db	181	VOGIITIRAAVYFGIYDTAKGMLPDEKNHIVISWMIACOTVTAVAGLTYSPEDDVRRMM	240
Oy	241	OSGRKGTDMTGTCLDDCAKRIARDGGKAAPFGAASNLRGCGAFVLYVDEIKKYT	298
Db	241	OSGRKGTDMTGTCLDDCAKRIARDGGKAAPFGAASNLRGCGAFVLYVDEIKKYT	298

RESULT 3
B43646
ADP,ATP carrier protein T2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C:Accession: B43646
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
Reference number: A43646; MUID:89229093

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M24103: NID:9529416: PIDN:AAA30769_1: PID:9529417
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat
K:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	94.2%;	Score 1458;	DB 2;	Length 298;
Best Local Similarity	92.9%;	Pred. No. 1.5e-121;		
Matches 275;	Conservative 13;	Mismatches 8;	Indels 0;	Gaps 0

[illegible]

RESULT
S03894

A:ADP,ATP carrier:protein T3 - human
N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:8926396
A:Accession: S03894
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level
A:Reference number: A94197; MUID:86124845
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
A:Experimental source: liver
A:Genetics:
A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: XP22.32-XP22.32; YP11.3-YP11.3
A:Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

	94.0%	Score 1454	DB 1	Length 298	
Query Match					
Best local Similarity	92.6%	Pred.	No. 3.4e-121		
Matches 274; Conservative 13;				Indels 0	Gaps 0
QY					
1	MIDALSPKDDLAGVAAAIKSTAVAPLIERKKLLQVOHASQTADNDQYKIICDQVR	60			
:	: : : : : : : : : :				

```

Db      1 MTEQALSFADFLAGGIAAISKTAVAPIERVKLLLOVQHASKOIADAKOYKGIIVDCIVR 60
OY      61 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
        61 IPKEQGLSVFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
OY      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
        121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
Db      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
OY      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
        181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
Db      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
OY      241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 296
        241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 296
Db      241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 296

RESULT      5
XMB0
ADP,ATP carrier protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Nov-1983 #sequence,revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24822; A03181; A61343; S69369
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
BiochemJ 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:89229093
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POW>
A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
R:Rasmussen, U.B.; Mohlrad, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A:Reference number: A24822; MUID:86295775
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>
A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
R:Aquila, H.; Mistr, D.; Eulitz, M.; Kilgenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A03181; MUID:82188267
A:Accession: A03181
A:Molecule type: protein
A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AOU>
A:Note: residue 52 may be methyllysine
R:Babel, W.; Wachter, E.; Aquila, H.; Kilgenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A:Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitochondrion
A:Reference number: A61343; MUID:82046808
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oetmeier, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A:Title: [(3H)-7-azido-4-Isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A:Reference number: S69369; MUID:95172058
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63;154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
C:Complex: homodimer
C:Function:
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A:Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochon
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

```

```

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:2/Modified site: acetylated amino end (Ser) (In mature form) #status experimental
F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match      91.7%; Score 1419; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 4,36-118;
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Db      1 MTEQALSFADFLAGGIAAISKTAVAPIERVKLLLOVQHASKOIADAKOYKGIIVDCIVR 60
        1 MSDQALSLKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
OY      61 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
        61 IPKEQGLSVFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
Db      61 IPKEQGLSVFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
OY      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
        121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
Db      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
OY      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
        181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
Db      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
OY      241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 297
        241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 297
Db      241 QSGRKGDIWYTGTLDCWRKIARDGCGKAFKGMNSVNLKMGCAFVLVLYDEIKK 297

RESULT      6
S37210
ADP,ATP carrier protein T1 - mouse
N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence,revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37210
R:Laplace, C.; Costel, P.
submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <LAP>
A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
C:Genetics:
A:Gene: ANCL1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match      91.6%; Score 1417; DB 2; Length 298;
Best Local Similarity 89.6%; Pred. No. 6,56-118;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Db      1 MTEQALSFADFLAGGIAAISKTAVAPIERVKLLLOVQHASKOIADAKOYKGIIVDCIVR 60
        1 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
        1 MGDQALSLKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVRR 60
OY      61 IPKEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
        61 IPKEQGLSVFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
Db      61 IPKEQGLSVFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRRQFMRFFAGNLASG 120
OY      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
        121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
Db      121 GAAGATSLCFVYPLDFARTRLAADVKGAGAEERERGLDCLVKIKYKSDGIGLYOGFNV 180
OY      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
        181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240
Db      181 VGGIITIRAAVFGYVDTRAKGMLPDPKNTHTIVISWIAQVTAVAGLTSYPEDTVRRRMM 240

```

Cy 241 QSGRKGTIMYTGTLDDCWRIKARDEGGKAFFKGAMSVNLRGMGFAVLVLYDEIKKY 297
 ||||| :|||
Lfb 241 QSGRKGADIMYTGTLDDCWRIAKDEGANAFKGAHSVNLRGMGFAFVLVLYLDEIKKY 297

RESULT 7
160173
adenine nucleotide translocator - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: 160173
R:Shinozuka, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A:Reference number: 160173; MUID:94002161
A:Accession: 160173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-298 <RES>
A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA3842.1; PID:g400427
A:Genetics:
A:Gene: anti
A:Introns: 37/3; 200/1; 247/1
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP/ATP carrier protein repeat homology <AC1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <AC2>
F:207-238/Domain: ADP/ATP carrier protein repeat homology <AC3>

Query Match	Similarity	91.6%	Score 1417	DB 2	length 298
Best Local	Similarity	89.6% <td>Pred. No. 6-5e-118</td> <td></td> <td></td>	Pred. No. 6-5e-118		
Matches	266	Conservative	16	Mismatches	15
				Indels	0
				Gaps	0
Q7	1	MTDALSPKDFPLAGVAAIAIKTAVAPIERYKLLIQVHASKQITADKQYGIIDCYVR	60		
Db	1	MDQDALSPKDFPLAGVAAIAIAVSKTAVAPIERKLLIQVHASKQISAEKQYGIIDCYVR	60		
Q7	61	IPKEQEVLSFEMGNLANVIRYFPTQALNFAFDKYKQIFLGGVDKRTQFQMFYFAGMLASG	120		
Db	61	IPKEQEVLSFEMGNLANVIRYFPTQALNFAFDKYKQIFLGGVDKRTQFQMFYFAGMLASG	120		
Q7	121	GAGAGTSLCFVPLDFAPRIPLADYVGKAGAEDEFKGLDGLVYKYSDEIKGLIYGFNWS	180		
Db	121	GAGAGTSLCFVPLDFAPRIPLADYVGKSGSOREFNLGDLTKIFKFSDELKGLIYGFNWS	180		
Q7	181	VGGIIIVRAAYFGIVDTAGMLPDPKNTHTIVISMIAQVTVTAVAGLTSPFPDVRRRMM	240		
Db	181	VGGIIIVRAAYFGIVDTAGMLPDPKNTHTIVISMIAQVTVTAVAGLTSPFPDVRRRMM	240		
Q7	241	QSGRGTDIMRTGILDCWRKIAIDBEGKAEFFGAGSNVLRGMGAFVLYLYDEIKY	297		
Db	241	QSGRGADIMRTGILDCWRKIAIDBEGKAEFFGAGSNVLRGMGAFVLYLYDEIKY	297		

A44778
ADP/ATP carrier protein T1 - human
A:Alternate names: mitochondrial ADP/ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778; S03893; A38691; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; MUID:89340499
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIR>
A:Cross-references: GB:J04982; NID:g178658; PIDN:AA51736.1; PID:g178659
R:Cozens, A.L.; Runswick, M.C.; Walker, J.E.

J. Mol. Biol. 006, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A>Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MUID:88041149
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'I', 228-298 <NEC>
A:CROSS-references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920
A:Experimental source: clone PHMANP
R:Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:CROSS-references: GB:J03593; NID:9339724; PIDN:AAA36751.1; PID:9339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1, T1
A:CROSS-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-89/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	91.3%	Score 1413	DB 1	Length 298
Best Local Similarity	89.2%	Pred. No. 1,5e-117		
Matches	265	Conservative	16	Mismatches 16; Indels 0; Gaps 0
QY	1	MTDALISFAKPLDLAGVAAAIKSTAVAPLERVKLLILOYHASKQITADKOYKGIIDCVVR	60	
Db	1	MDHMAWSEFLDKDLAGVAAAVASTAAPLERVKLLILOYHASKQISAEKOYKGIIDCVVR	60	
QY	61	IKREDEVLSFWMGNLANVIRYFPTQALNFAPFKDKYKQIPLGQVDRKTPQWFRFAGNLASG	120	
Db	61	IKREGEFLSFWMGNLANVIRYFPTQALNFAPFKDKYKQIPLGQVDRKTPQWFRFAGNLASG	120	
QY	121	GAGAGTSLCFVYPLDFAFRRLAADNGKAGABERFNSGLDCLVYKYSKDGIKGLYGFNWS	180	
Db	121	GAGAGTSLCFVYPLDFAFRRLAADNGKGAORFPHLGGCIIKIFSDSLRGLYGFNWS	180	
QY	181	VGGIITRYRAAYFGIYDTAKGMLPDPKNTAIIIVSIIMIAQVTVTAAGTSLYSPFDVRRRRMM	240	
Db	181	VGGIITRYRAAYFGVDTAKGMLPDPKNNHIIIVSMIIAQSVTAVAGLVSPFDVRRRRMM	240	
QY	241	QSGRKCTDIIMTGTLLDCWKKIARDEBGGKAFFGAMSNVLRGMGAFVLYLDEIKKY	297	
Db	241	QSGRKCADIMTGTLLDCWKKIARDEBAAKAFFGAMSNVLRGMGAFVLYLDEIKKY	297	

RESULT 9
S31935
ADP,ATP carrier protein - African malaria mosquito
C.Species: Anopheles gambiae (African malaria mosquito)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S31935: S31936
R.Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A.Description: A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles gambiae*
A.Reference number: S31935

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:33:11 ; Search time 57.26 Seconds

(without alignments)
385.502 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDAALSFADFLAGVAAA.....LRGMAFVLVDEIKKKT 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
A.Geneseq_1101:*

- 1: /SIDS8/gcgdata/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/AA1982.DAT:*
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- 21: /SIDS8/gcgdata/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	21	AAV71032 Human adenine nucl
2	1547	100.0	298	22	AAU01199 Human adenine nucl
3	1454	94.0	298	21	AAV71033 Human adenine nucl
4	1454	94.0	298	22	AAU01200 Human adenine nucl
5	1454	94.0	298	22	AAU01200 Human adenine nucl
6	1454	94.0	323	22	AAU41427 Human polypeptide
7	1411	91.2	298	19	AAW61169 Ant1 protein. Mus
8	1391.5	89.9	297	21	AAV71031 Human adenine nucl
9	1391.5	89.9	297	22	AAU01198 Human adenine nucl
10	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
11	747.5	48.3	346	21	AAU01198 Arabidopsis thajia

12	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
13	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
14	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
15	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
16	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
17	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
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19	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
20	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
21	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
22	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
23	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
24	747.5	48.3	346	21	AAU01198 Arabidopsis thajia
25	744.5	48.1	346	21	AAU01198 Arabidopsis thajia
26	744.5	48.1	346	21	AAU01198 Arabidopsis thajia
27	744.5	48.1	346	21	AAU01198 Arabidopsis thajia
28	741.5	47.9	346	22	AAU01198 Arabidopsis thajia
29	690.5	44.6	330	21	AAU01198 Arabidopsis thajia
30	687.5	44.4	330	21	AAU01198 Arabidopsis thajia
31	687.5	44.4	333	21	AAU01198 Arabidopsis thajia
32	687.5	44.4	350	21	AAU01198 Arabidopsis thajia
33	687.5	44.4	368	21	AAU01198 Arabidopsis thajia
34	660.5	42.7	291	21	AAU01198 Arabidopsis thajia
35	657.5	42.5	291	21	AAU01198 Arabidopsis thajia
36	655	42.3	306	21	AAU01198 Arabidopsis thajia
37	655	42.3	306	21	AAU01198 Arabidopsis thajia
38	637	41.2	291	21	AAU01198 Arabidopsis thajia
39	637	41.2	291	21	AAU01198 Arabidopsis thajia
40	585.5	37.8	249	21	AAU01198 Arabidopsis thajia
41	582.5	37.7	249	21	AAU01198 Arabidopsis thajia
42	574.5	37.1	312	21	AAU01198 Arabidopsis thajia
43	570.5	36.9	263	21	AAU01198 Arabidopsis thajia
44	570.5	36.9	263	21	AAU01198 Arabidopsis thajia
45	565.5	36.6	228	21	AAU01198 Arabidopsis thajia

ALIGNMENTS

RESULT 1	
AAV71032	standard; Protein: 298 AA.
XX	AAV71032:
AC	AAV71032:
XX	29-AUG-2000 (first entry)
DE	Human adenine nucleotide translocator ANT2.
XX	Human: adenine nucleotide translocator: ANT2; mitochondria: ADP: ATP.
KW	adenosine di-phosphate: adenosine tri-phosphate: apoptosis: MPT: cancer:
KW	mitochondrial permeability transition: neuroprotective: neurotropic:
KW	antiparkinsonian: cytoskeletal: antidiabetic: anticonvulsant: neuroleptic:
KW	antipsoriatic: cerebroprotective; therapeutic: screening; psoriasis:
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes: Leber's hereditary optic neuropathy: schizophrenia; MELAS;
KW	mitochondrial encephalopathy: lactic acidosis: stroke: MIDD:
KW	mitochondrial diabetes and deafness: hyperproliferative disorder:
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
XX	
PN	MO200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	
PR	08-SEP-1999; 99US-0393441.
XX	
PA	(MITO-) MITOKOR.
XX	

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 PI Ghosh SS;
 XX
 DR MPI; 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SO Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1,1e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDLVAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCVR 60
 DB 1 mtdaalstfkdllagvaaaistavapieryklllyqhaskqitadkqygiidcvr 60
 QY 61 IPKEQEVLSFMWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFFAGNLASG 120
 DB 61 lpkegevisfwrnglanviryftqalnfafkdkyqiflgvdkrtqwrffagnlasg 120
 QY 121 GAAGATSLCFVVPDLPARTRLADYVGKAGAEERFGLDCLVKIKYKSDGINKLYGCFNVS 180
 DB 121 gaagatslcfvvpdlpartrladvygkagaeerfglgclvkiyksdgi klygcfnvs 180
 QY 181 VGGIIRAAVYRGIVDTAGMLPDKNTHIVISWMAQVTVAVAGTSTPFTVRRMM 240
 DB 181 vggiiiraaavyrgivdtagmlpdknthiviswmaqlvtavagltstypftvrrmm 240
 QY 241 OSGRKGTDMYTGTDLCWKRKIADEGKAFKFGAMSNVLRGGAFAVLVLYDEIKKYT 298
 DB 241 osgrgtldmytgtdlcwkrkiardegkafkfgamsnvlrsggafvlylydeikkyt 298

RESULT 2
 ID AAU01199 standard; Protein; 298 AA.
 AC AAU01199;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX..

OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Vellicelebi G, Davis RE;
 XX
 DR MPI; 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SO Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1,1e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDLVAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCVR 60
 DB 1 mtdaalstfkdllagvaaaistavapieryklllyqhaskqitadkqygiidcvr 60
 QY 61 IPKEQEVLSFMWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFFAGNLASG 120
 DB 61 lpkegevisfwrnglanviryftqalnfafkdkyqiflgvdkrtqwrffagnlasg 120
 QY 121 GAAGATSLCFVVPDLPARTRLADYVGKAGAEERFGLDCLVKIKYKSDGINKLYGCFNVS 180
 DB 121 gaagatslcfvvpdlpartrladvygkagaeerfglgclvkiyksdgi klygcfnvs 180
 QY 181 VGGIIRAAVYRGIVDTAGMLPDKNTHIVISWMAQVTVAVAGTSTPFTVRRMM 240
 DB 181 vggiiiraaavyrgivdtagmlpdknthiviswmaqlvtavagltstypftvrrmm 240
 QY 241 OSGRKGTDMYTGTDLCWKRKIADEGKAFKFGAMSNVLRGGAFAVLVLYDEIKKYT 298
 DB 241 osgrgtldmytgtdlcwkrkiardegkafkfgamsnvlrsggafvlylydeikkyt 298

RESULT 3
ID AAY71033 standard; Protein; 298 AA.
XX AAY71033:
XX AAY71033:
XX 29-AUG-2000 (first entry)
XX
XX Human adenine nucleotide translocator ANT3.
DE
XX
XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotropic;
KW antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
KW antiproliferic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200026370-A2.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-US25883.
PF
XX
XX 03-NOV-1998; 98US-0185904.
PR 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
PA
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
PI WPI: 2000-365619/31.
DR N-PSDB: AAD00521.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
PT
XX
XX Claim 46; Page 173-174; 175pp; English.
PS
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial pore function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA:

[illegible]

Db	1	mtgagisfakbfllagglglaaaistcaavpiervkllllqvghaskqjaadkkykivdcivcr	60
Qy	61	IPKEDEVLSEPMKGNLANVIRYEPQALNFAEKDKYKQIPLGVDKRTQEMRYEAGNLASG	120
Db	61	ipkegvvisfwrgrlanviryfpcqalnfaekdkykyqilfgyvdkhbqfwrtyfagnnag	120
Qy	121	GAAGTSTSCFYVPIIDPEARTRLAAVGVKAGAREPRRGIDGLVTKYKSDGIKGICYOPNNS	180
Db	121	gaagtsctcyvpidfactrilaadvagskgeterfrygdcivkrlktsdgrltyfyqgsvs	180
Qy	181	VGGIIIVRAAYFGIYDTAKGMLDPKKTHIVISWIAQOTYAAVAGLSTPEFDYRRRRMM	240
Db	181	vqgiiivyaayfygydteakgmldppkthiavswiaqvctvavagvsygfdeivrrrrmm	240
Qy	241	OSGRKGTIDINTGRLDCCRKRTARDEGSKAPFKGMSVNLGMSGAPVLYLYIDEIKK	296
Db	241	osgrtgdalmylgtvdcwrkltridegskafkgsavswlrlgmgaivtlvlyideikk	296

RESULT	4
AAM39641	standard; Protein; 298 AA.
XX	
AC	AAM39641;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 2786.
XX	
KM	Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM	peripheral nervous system; neuropathy; central nervous system; CNS;
KM	Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
KM	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KM	leukemia.
XX	
OS	Homo sapiens.
XX	
PN	WO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000MO-US34263.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	
DR	WPI: 2001-442253/47.
DR	N-PSDB: AA158797.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Example 4; SEQ ID NO 2786; 10078pp; English.
XX	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and

PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB: AA160383.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 2; SEQ ID NO 6358; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA38642-AA42213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activity/inhibit activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 323 AA:
SO
Query Match 94.0%; Score 1454; DB 22; Length 323;
Best Local Similarity 92.6%; Pred. No. 7, 8e-145;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
OY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
26 mteqalsifakdfilaggaiaaistavapiervklllqvghaskqiaadkqygiidcvr 85
OY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGCVKRPQFMRYFAGNLASG 120
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
86 lpeqgvlstfwrgrlanviryfpcqalnfaikdkyqgflfgvdkhkfwyfagnlasg 145
OY 121 GAAGATSLCFVYPLDFAFTRILADVKGAGAEERFRGLGDCLVKTKYKSDGKGLYQGFNVS 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
146 gaagatslcfvypldfarttrilaadvkgsgeretrgldcvlktksdglrtgylqgfsvs 205
OY 181 VQGIITIRAAVFGIYDTAKGMLPDKMTHVISMIAQVTAAGLTSYPTDVRRRMM 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
206 vvgllllyraayfgvydtkagmlpdkmthlvswmlaqvtavagvvsypdltvrrmm 265
OY 241 QSGKGGDIWYTGTLDCWRKRIARDEGKAPFKGAMSVNLRGMGAFVLVYDEIKK 296
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
266 qsgkggdiwytgltcdwrcrkifrdggaikafkgaamsvnlrgmgafvlvlydelkk 321

RESULT 7
AAW61169
ID AAW61169 standard; Protein; 298 AA.
XX
XX AAW61169;
AC
XX
DT 28-SEP-1998 (first entry)
XX
DE Anti protein.
XX
XX Anti1; Adenine nucleotide translocator; cloning; screening;
KW DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe: OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
XX Mus sp.
OS
XX
XX W09819714-A1.
PN
XX
XX 14-MAY-1998.
PD
XX
XX 31-OCT-1997; 97MO-US19882.
PE
XX
XX 01-NOV-1996; 96US-0030017.
PR
XX
XX (UYEM-) UNIV EMORY.
PA
XX
XX Graham BC, Macgregor GR, Wallace DC;
PI
XX
DR WPI: 1998-286608/25.
DR N-PSDB: AAV36479.
XX
PT Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
PS Disclosure; Page 39-40; 61pp; English.
XX
XX The present sequence is the mouse Anti1 protein, the cDNA producing this
XX polypeptide is cloned by screening a mouse heart cDNA library with the
XX human Anti1 cDNA as a probe. The Anti1 cDNA sequence was determined by DNA
XX Tag diodeoxy terminator cycle sequencing. The Anti1 protein is encoded by
XX CC the Anti1 locus, a nuclear gene on chromosome 8. This protein is required
XX in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
XX which can then be converted into ATP. An Anti1 homozygous mutant would
XX CC thus be defective in OXPHOS which results in disease in oxidative
XX metabolism dependent tissues. This mouse Anti1 homozygous mutant can be
XX used as a model system for fascioscapular humeral muscular dystrophy,
XX hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
XX CC systems can be used to test possible therapeutic compounds which
XX increase/mediate ATP and ADP exchange across the mitochondrial membrane
XX independent of Anti1.
XX
XX Sequence 298 AA:
SO
Query Match 91.2%; Score 1411; DB 19; Length 298;
Best Local Similarity 89.2%; Pred. No. 2, 4e-140;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
OY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
1 mtdaaislfakdfilaggaiaaistavapiervklllqvghaskqiaadkqygiidcvr 60
OY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGCVKRPQFMRYFAGNLASG 120
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
61 ipkeqgvlstfwrgrlanviryfpcqalnfaikdkyqgflfgvdkhkfwyfagnlasg 120
OY 121 GAAGATSLCFVYPLDFAFTRILADVKGAGAEERFRGLGDCLVKTKYKSDGKGLYQGFNVS 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 121 gaagatslcfvypldfartllaadvkgsqsfnglgclikfkfsdglxlygqfsvs 180
Qy 181 VGGIIYRAAYGIVDTAKGMLPDPKNTHTIVISWMTAQTAVAGLTSYPTFVRRRMW 240
Db 181 vggililyraayfgvydtaqgmldpdknvhlivswwlaqsvtavagllsyptdvtvrrmm 240
Qy 241 OSGRKGTDMVTGTLDCWKRRIARDEGKAFFKGAMSNVLRGAGFVLVYEIKKY 297
Db 241 gsgrrkgtadlmvgtdcwrkriakdegakafkfgawsnvlrimgsfatvlylyeikky 297

RESULT 8

AAU01198
ID AAU01198 standard; Protein: 297 AA.

AAU01198

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANTL.

Human: adenine nucleotide translocator: ANTL; mitochondria: ADP: ATP;
adenosine di-phosphate: adenosine tri-phosphate; apoptosis: MPT: cancer;
mitochondrial permeability transition; neuroprotective; noctropic;
antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
mitochondrial diabetes and deafness; hyperproliferative disorder;
myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

WO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0393441.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;

WPI: 2000-365619/31.

N-PSDB: AAD00519.

Recombinant construct encoding adenine nucleotide translocator
polypeptide, useful e.g. in screening for potential therapeutic agents
against mitochondrial disease

Claim 44; Page 172; 175pp; English.

The patent discloses a method to produce adenine nucleotide translocator
(ANT) proteins or ANT fusion proteins using recombinant expression of
constructs. ANT is a nuclear encoded protein and a major component of
inner mitochondrial membrane. It mediates transport of adenosine
di/tri-phosphates across the mitochondrial inner membrane and also serves
as an important molecular component of the mitochondrial permeability
transition pore, a modulator of apoptosis. ANT is used to identify agents
or ligands that bind to, or interact with it. The ANT ligands are used to
detect or isolate ANT in a biological sample, and therapeutically for
regulating mitochondrial pore activity, for treating diseases associated
with altered mitochondrial function, including Alzheimer's, Parkinson's
and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
epilepsy red ragged fibre syndrome. The present sequence is an

CC adenine nucleotide translocator ANTL from human brain.
XX
SQ Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 21; Length 297;
Best Local Similarity 88.6%; Pred. No. 2.7e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MTDALSFAPKDFLAGVAATKSTNAPLIERKLLLOVHASKOITADBOYGIIDCYVR 60
Db 1 mgdhwstlkdlagavaavsktavaplerklllqvhasqsaekqxlidcavr 60
Qy 61 IPKDEVLSEFMRGNLANVIRYPTQALNFAFDKYKQIFLAGGVDRKTPFRFAGNLASG 120
Db 61 ipkegflsfwrnlanvlyrftgalnfafdkyqqlilgvgdrkqkqfwrfaenlaag 120
Qy 121 GAAGATSLCFVYPLDFARTRLAADVGKAGAEERFGLSDCLVKYKSDGIKGLYGFNV 180
Db 121 gaagatslcfvypldfartllaadvgr-agsrefnglgclikfkfsdglrlygqfsvs 179
Qy 181 VGGIIYRAAYGIVDTAKGMLPDPKNTHTIVISWMTAQTAVAGLTSYPTFVRRRMW 240
Db 181 vggililyraayfgvydtaqgmldpdknvhlivswwlaqsvtavagllsyptdvtvrrmm 239
Qy 241 OSGRKGTDMVTGTLDCWKRRIARDEGKAFFKGAMSNVLRGAGFVLVYEIKKY 297
Db 241 gsgrrkgtadlmvgtdcwrkriakdegakafkfgawsnvlrimgsfatvlylyeikky 296

RESULT 9

AAU01198
ID AAU01198 standard; Protein: 297 AA.

AAU01198

07-SEP-2001 (first entry)

Human adenine nucleotide translocator-1 (ANT-1) protein.

Human: adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;
mitochondrial permeability transition pore component; cell survival;
mitochondrial core component; mitochondrial related disorder; cancer;
Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

Homo sapiens.

WO200132876-A2.

10-MAY-2001.

03-NOV-2000; 2000WO-US30535.

03-NOV-1999; 99US-0434354.

(MITO-) MITOKOR.

Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Velicelebi G, Davis RE;

WPI: 2001-291054/30.

N-PSDB: AAS05901.

New nucleic acid expression constructs, useful for screening for agents
that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
fused to energy transfer molecule

Disclosure; Fig 2; 186pp; English.

The present sequence represents human adenine nucleotide translocator-1
(ANT-1) protein. ANT proteins are mitochondrial permeability
transition (MPT) pore components responsible for mediating transport

[illegible]

PR	13-OCT-1999;	99US-0155293.
PR	13-OCT-1999;	99US-0155294.
PR	13-OCT-1999;	99US-0155295.
PR	14-OCT-1999;	99US-0155329.
PR	14-OCT-1999;	99US-0155330.
PR	14-OCT-1999;	99US-0155331.
PR	14-OCT-1999;	99US-0155637.
PR	14-OCT-1999;	99US-0155638.
PR	18-OCT-1999;	99US-0155584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

OY		7	SNAKDELGAGVAAAIASKTAVAPIERUKILLLOYOHASKOTA---DKQYGIIDCVVRIRK	63
Dd		44	.. : :	101
OY		64	BGEVLSFPMGNLANIYRYPEPTOALNPAFKDKKOIFLGVDNRTOEPMRFAGNLASGAA	123
Dd		102	déqfsglsygnntanyirfpqalnfaIdkfkrllnfkkd~rdgywkwfagqlasgaa	160
OY		124	GATSLCFPVPLDFAARTRLAAD---VGKAGAEERFNGLDCLVIKYSDSdIKGLYOGENFS	180
Dd		161	gasalllfysldatcrrlendaakaakggggqfgglvayvk~kllktgdlaglyrgfnls	220
OY		181	VGGITTYRAAYRGICYDTAK----GMLPDPKNTHYIVSMIAOTVTAVAGLTSYPEDTVR	235
Dd		221	cvglllvryglfyglvdsvkvpllltgdldgsffasfalgvvl----tnngslasydpdtvr	276
OY		236	RMMMQSGKKGRDIWYTGTGLDCMRKIARDEGSKAFPKGMSVNLRCMGAFVLVLYDEL-	294
Dd		277	rmmmtutsgea---vkyssldaIfkgllknegaksIlkfgaganllravagaylsydklq	333
OY		295	-----KKY 297 	
Dd		334	llvfqky 341	
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XX	DT	18-OCT-2000	(first entry)	
XX	DE	Arabidopsis thaliana	protein fragment SEQ ID NO:	45788.
KW	protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
OS	termination sequence.			
OS	Arabidopsis thaliana.			

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PR 29-OCT-1999; 990S-0162142.

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Best Local Similarity 53.9%; Pred. No. 2.3e-70;
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DB 44 nfaIdtflmgysaavsktaapierkvklllqng--demlkagrlsepykgidcftllk 101
OY 64 EDEVLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTFOFRYFAGNLASGGA 123
DB 102 degfsglwtgrntanvlyrftqelnfakdyekrlfnfkcd-rdykwkfaaglaasgaa 160
OY 124 GATSLCEFYVRIDFARTRLAAD--VGKAGAEERFEGRLGCLIVYKSDGKGLXGEPNS 180
DB 161 gassllfvsldyartllandakaakkggggrtfgldvdyrftllcdgnaqlrygfnls 220
OY 181 VOGIIRAYAFGIYDTAK-----GMLPRKNTNIIYSMMIAQTVAVAGLTSYPRDTVA 235
DB 222 cvglllyrlyfgyldsvprvlltgdldgsffasfalgwli-----lngslasryldtvt 276
OY 236 RRMAMOSGRKGTIDMYTGTIDCWKRTARDEGSKAFKGSANVLKRMGAFLVLYDEI- 294
DB 277 rrrmmmsgsa---vkysksidafkqllknegaksllkgsaganllravagavlsydydkl 333
OY 295 -----KKY 297
DB 334 llyvfgkky 341

RESULT 12
AAG37264

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AC AAG37264;
XX 18-OCT-2000 (first entry)
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
XX Arabidopsis thaliana
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PN EP1033405-A2.
XX 06-SEP-2000.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.3%; Score 747.5; DB 21; Length 346;
Best Local Similarity 53.9%; Pred. No. 2.3e-70;
Matches 166; Conservative 38; Mismatches 77; Indels 27; Gaps 8;
7 SFAKDLGAGVAAIAISKTAVAPIERVKLLQVOHASKQITA---DKQYKGIIDCVVRIPK 63

Db 44 nfaIdflmgvsaavsktaapiervklIlgnq--demikagrlsepykglgdcfgtlik 101
Oy 64 EOEYLSFRGNLANVIRFPFQALNFAFKDKYKOIFLGGVDKRFQFRRYFAGNLASGAA 123
Db 102 degfsglwrntanvilyfclqalnfaikdyfkrIfnfxkd-rdgykkwfagnlasgaa 160
Oy 124 GATSLCFVYPLDFARFRLAAD---VGKAGAEERERCGDCLVKYKSDGJKGLVQGNVS 180
Db 161 gaslllfvysldyartllandakaakkggggqldglvdvyrrklkcdglaglyrgfnls 220
Oy 181 VOGIIYRAAYFCIYDPAK-----GMLPDPKNTIIVSMIAQTVAAGLTSYPTFVR 235
Db 221 cvglivryglyfglydsvkpvlIlgdlqdsffasfaIgwI----tngaglasypIdtvr 276
Oy 236 RRMMOSGRKGTDMYGTLDCKWRKIRADBGKAFKFGANSNVLRKGAFVLVLYDEI- 294
Db 277 rrmmtsgaa---vkyksIdafkqIlknegakslfkfgaganaIlIrvagagvlsqykIq 333
Oy 295 -----KKY 297
Db 334 IIVfGkky 341
RESULT 14
AAG36576
ID AAG36576 standard; Protein: 363 AA.
XX AAG36576;
AC
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44844.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0138459.
PR 18-JUN-1999; 99US-0138460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 29-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141844.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144886.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:34:15 ; Search time 55.37 Seconds
(without alignments)
787.234 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQSAISFADFLAGIAA.....LRGGAFLVLYDELKKVI 298

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_TREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1422	92.2	298	6	046373
2	1421	92.1	298	13	0919M9
3	1418	91.9	298	11	062164
4	1409	91.3	298	13	Q9PRH1
5	1406	91.1	298	13	Q9PRH2
6	1402	90.9	298	13	Q9YIC4
7	1259	81.6	317	13	Q91336
8	1235.5	80.1	300	5	Q9NHM5
9	1187.5	77.0	288	5	044093
10	1183.5	76.7	288	5	044094
11	1176.5	76.2	304	5	Q25129
12	1137.5	73.7	307	5	062526
13	1119	72.5	315	4	Q9H0C2
14	1041	67.5	313	5	Q21103
15	1039	67.3	313	5	P91410
16	1038	67.3	300	5	045865
17	996	64.5	309	5	097470
18	993.5	64.4	300	5	001813
19	993	64.4	300	5	017407

20	973.5	63.1	318	5	09B36
21	946.5	61.3	307	8	09XM22
22	944	61.2	301	5	025692
23	943	61.1	301	5	026006
24	827	53.6	170	6	09XS69
25	778.5	50.5	305	3	09P8M1
26	764	49.5	326	5	P91270
27	760	49.3	307	5	076286
28	759	49.2	303	3	074260
29	756.5	49.0	306	5	016683
30	753	48.8	307	5	026697
31	750.5	48.6	385	10	Q9FY52
32	747	48.4	306	3	P78754
33	744	48.2	388	10	049875
34	743	48.2	379	10	049447
35	743	48.2	386	10	P93767
36	734	47.6	331	10	041628
37	731.5	47.4	305	3	09P876
38	731	47.4	317	5	09N647
39	728.5	47.2	305	3	09P875
40	688.5	44.6	330	10	09PM86
41	681.5	44.2	298	5	021809
42	653.5	42.4	262	10	09AV76
43	520.5	33.7	327	10	09LF44
44	500.5	32.4	162	5	026130
45	441.5	28.6	158	5	076467

ALIGNMENTS

RESULT 1
ID 046373 PRELIMINARY: PRT: 298 AA.
AC 046373;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Granulata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKLETAL MUSCLE;
RA Yamaguchi N., Kasai M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: NO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB009386; BAA23777.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mitl_carrier.
DR Pfam: PF00153; mitl_carrier. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 32901 MW: CAEA32C8B164AD78 CRC64;

Query Match 92.2% Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 6.9e-122;
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;
QY 1 MTEQSAISFADFLAGIAAISKTAAPIERVKLLQVHASRQIAADKQKGIQVDCIVR 60
DB 1 MSQQAISFLKDFLAGVAAVSKTAVAPIERVKLLQVHASRQISAEKQYGIQDCIVR 60
QY 61 IPEQGYLSFWRGNLANVIRYFTQALNFAFKQYKQIFLGVDKHTQFRRYRAGNLASG 120
DB 61 IPEQGYLSFWRGNLANVIRYFTQALNFAFKQYKQIFLGVDKHTQFRRYRAGNLASG 120

QY 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 DB 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 QY 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298
 DB 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298

RESULT 2
 Q919M9 PRELIMINARY; PRT; 298 AA.
 AC Q919M9:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADENINE NUCLEOTIDE TRANSLOCASE.
 GN ANTI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression during Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL, AF231347; AAF63471.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MITOCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;
 SQ

Query Match 92.1%; Score 1421; DB 13; Length 298;
 Best Local Similarity 90.3%; Pred. No. 8.6e-122;
 Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADADKQYGVDCIYR 60
 DB 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADADKQYGVDCIYR 60
 QY 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 DB 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 QY 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298
 DB 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298

RESULT 3
 Q62164 PRELIMINARY; PRT; 298 AA.
 AC Q62164:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR
 DE TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE
 DE TRANSLOCATOR), MEMBER 4).
 GN SLC25A4 OR MANCI OR ANTI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=MUSCLE;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL, X74510; CA652616.1; -;
 DR EMBL, AF240002; AAF64470.1; -;
 DR EMBL, BC003791; AAH03791.1; -;
 DR MGD, MGI:1353495; SLC25A4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;
 SQ

Query Match 91.9%; Score 1418; DB 11; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1.6e-121;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADADKQYGVDCIYR 60
 DB 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADADKQYGVDCIYR 60
 QY 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFMGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYPLDFAFTRRLADYVGKSGTEREFGLDCLVTKIRKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 DB 181 VGGIITVAAAFGVYDFAKGMIPDPKNTNHIYVSMIAOTVTAAGVSYPPFTVRRMM 240
 QY 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298
 DB 241 OSGRKGADIMTYGVDCKRKIFRDEGKAFFKGANSNVLKRGGAFFVLVLYDELKVI 298

RESULT 4
 Q9PRH1

ID 09PRH1 PRELIMINARY: PRT: 298 AA.
AC 09PRH1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase.";
RT Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008463; BAA36513.1; -;
DR EMBL: AB008456; BAA36506.1; -;
DR EMBL: AB008461; BAA36511.1; -;
DR EMBL: AB008462; BAA36512.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; MitC_carrier.
DR InterPro: IPR002030; MitC_uncoupling.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUOCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F54BD36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 1,1e-120;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MPEQAIKFAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIADKQKIVDCIYR 60
DB 1 MDDAISFAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOIADKQKIMCVR 60
QY 61 IPKEQGVLSFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRVAGNLASG 120
DB 61 IPKEQGVLSFWKGNLANVIRFPTQALNFAFKDKYKIFLDNDKRTQFWRVAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADAVGKSTEREFRGIGDCLVKTFSKDGIRGLYGFSSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADAVGKADREFKIGDCLAKIFKSDGLKGLYGFNVS 180
QY 181 VQGIITIRAAVFGVDTAKGMPLDPKNTHTFISWMIATQVTAAGVAFSTPFDIVRRMM 240
DB 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTFISWMIATQVTAAGVAFSTPFDIVRRMM 240
QY 241 QSGRKADIMYTGTCVQWKRIFRDEGKAFKGAWSNVLRGKGAPVLVYDELKTYI 298
DB 241 QSGRKAEIMYSGTIDCWKRIARDEGSRAPFKGAMSNVLRGKGAPVLVYDELKTYI 298
RESULT 5
09PRH2 PRELIMINARY: PRT: 298 AA.
AC 09PRH2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8410;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase.";
RT Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008460; BAA36510.1; -;
DR EMBL: AB008458; BAA36508.1; -;
DR EMBL: AB008459; BAA36509.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; MitC_carrier.
DR InterPro: IPR002030; MitC_uncoupling.
DR Pfam: PF00153; mito_carrier_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUOCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599406 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 2e-120;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MPEQAIKFAKDFLAGGIAAISTAVAPIERVKLLQVQHASKOIADKQKIVDCIYR 60
DB 1 MDDAISFAKDFLAGGVAIAISKTAVAPIERVKLLQVQHASKOIADKQKIMCVR 60
QY 61 IPKEQGVLSFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRVAGNLASG 120
DB 61 IPKEQGVLSFWKGNLANVIRFPTQALNFAFKDKYKIFLDNDKRTQFWRVAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADAVGKSTEREFRGIGDCLVKTFSKDGIRGLYGFSSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADAVGKADREFKIGDCLAKIFKSDGLKGLYGFNVS 180
QY 181 VQGIITIRAAVFGVDTAKGMPLDPKNTHTFISWMIATQVTAAGVAFSTPFDIVRRMM 240
DB 181 VQGIITIRAAVFGIYDTAKMLPDPKNTHTFISWMIATQVTAAGVAFSTPFDIVRRMM 240
QY 241 QSGRKADIMYTGTCVQWKRIFRDEGKAFKGAWSNVLRGKGAPVLVYDELKTYI 298
DB 241 QSGRKAEIMYSGTIDCWKRIARDEGSRAPFKGAMSNVLRGKGAPVLVYDELKTYI 298
RESULT 6
09YIC4 PRELIMINARY: PRT: 298 AA.
AC 09YIC4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
a sex-linked gene, ADP/ATP translocase.";
RT Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

DR EMBL; AB008457; BAA36507.1; -
DR InterPro: IPR001993; Mitochond_carrler.
DR InterPro: IPR002067; Mit_carrler.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
Best Local Similarity 87.9%; Pred. No. 4.7e-120;
Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERKLLQVQHASKOIADKQYKGYDCTVR 60
DB 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERKLLQVQHASKOITADKQYKGYDCTVR 60
OY 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
DB 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
OY 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
OY 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
OY 181 VOGIIYRAAFGVYDTPAKGMLPDKNTHIVSWMIATQVTVAAGVSYPDYVRRMM 240
DB 181 VOGIIYRAAFGVYDTPAKGMLPDKNTHIVSWMIATQVTVAAGVSYPDYVRRMM 240
OY 241 OSGRKGAIDMTGTVDCKRKIFRDEGKAFKFGKAMSNNLRGNGAFVLYVDELKKVI 298
DB 241 OSGRKGAIDMTGTVDCKRKIFRDEGKAFKFGKAMSNNLRGNGAFVLYVDELKKVI 298

RESULT 7
091336 PRELIMINARY; PRT; 317 AA.

ID 091336
AC 091336;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana sylvatica (wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=97398141; PubMed=9256066;
RA Cai O., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
in wood frogs under freezing stress";
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP REVISIONS.
RP Cai O., Storey K.B.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
-1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; U44832; AAB97882.2; -
DR InterPro: IPR001993; Mitochond_carrler.
DR InterPro: IPR002067; Mit_carrler.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F66B7EDBD5CB872 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 6e-107;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERKLLQVQHASKOIADKQYKGYDCTVR 60
DB 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERKLLQVQHASKOITADKQYKGYDCTVR 60
OY 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
DB 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
OY 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
OY 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
DB 121 GAAGATSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVS 180
OY 181 VOGIIYRAAFGVYDTPAKGMLPDKNTHIVSWMIATQVTVAAGVSYPDYVRRMM 240
DB 181 VOGIIYRAAFGVYDTPAKGMLPDKNTHIVSWMIATQVTVAAGVSYPDYVRRMM 240
OY 241 OSGRKGAIDMTGTVDCKRKIFRDEGKAFKFGKAMSNNLRGNGAFVLYVDELKKVI 298
DB 241 OSGRKGAIDMTGTVDCKRKIFRDEGKAFKFGKAMSNNLRGNGAFVLYVDELKKVI 298

RESULT 8
09NHWS PRELIMINARY; PRT; 300 AA.

ID 09NHWS
AC 09NHWS;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS MAL SEEKING;
RA Chen Z., Fair J.A., Batterham P.;
RT "A cDNA clone encoding the ADP/ATP translocase of Lucilia cuprina.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
-1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAB32322.1; -
DR InterPro: IPR001993; Mitochond_carrler.
DR InterPro: IPR002067; Mit_carrler.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 80.1%; Score 1235.5; DB 5; Length 300;
Best Local Similarity 79.5%; Pred. No. 7.7e-105;
Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

OY 6 ISFANDFLAGGIAAISTKAVAPIERKLLQVQHASKOIADKQYKGYDCTVRIPKEQ 65
DB 9 LGFVDFDAAGGISAIVSTAVAPIERKLLQVQHASKOISPDKQYKGYDCTVRIPKEQ 68
OY 66 GYLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSGAGA 125
DB 66 GYLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSGAGA 128
OY 126 TSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVOCIT 185
DB 129 TSLCFYVPLDFARTRLADYGVKSGTEREFGLDCLVKTYSKDGIRGLYOGFSVOCIT 187


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OY 186 IYRAAFGVYDPAKGLPDPKNTHTIVSMIAOTYTAAGVSVPPDTVRRMMMSGRK 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 IYAAAFGFDPTARGLPDPKNTHTIVSMIAOYTTVACIVSPEDTVRRMMMSGRK 247

OY 246 GADIMYTGVDGWRKIFRDEGKAFKAGMSNVLRMGAFVLVLDLKKVI 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 248 AFEIIVKNTLHCWATIAKOGEGTCAFFKAGAFSNVLRGGAFAVLVLDLKKFL 300

RESULT 9
O44093 PRELIMINARY: PRT; 288 AA.
ID 044093:
AC 044093:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE (FRAGMENT).
GN SESB.
OS Drosophila pseudobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN (1)
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -I- INNER MEMBRANE (BY SIMILARITY).
CC -I- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025798; AAB87883.1; -.
DR FlyBase: FBgn0023292; Dros\sesb.
DR InterPro: IPR001993; Mitoch\_carrier.
DR InterPro: IPR002067; Mit\_carrier.
DR Pfam: PF00153; mito\_cartr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH\_CARRIER. 3.
DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC05043680 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
Best Local Similarity 80.7%; Pred. No. 1.8e-100;
Matches 220; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

OY 5 AISFADFLAGIAAISKTAVALPIERVKLLQVHASKOIADKOYKGVDCIVRIPIKE 64
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 7 AIGFVDFDFAAGISAAVSKAVALPIERVKLLQVHISKOISPDKOYKGVDCIVRIPIKE 66

OY 65 QGVLSTWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 124
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 QGFSSTWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 126

OY 125 ATSLCFEYVPLDFARTRLADVGKSGTEREFGGLDCLVITKSDGIRGLYQGFVSVOGI 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 ATSLCFEYVPLDFARTRLADVGKSG- QREFTGLGNCLTKIFKSDGLVGLYRGFVSVOGI 185

OY 185 IYRAAFGVYDPAKGLPDPKNTHTIVSMIAOYTTAAGVSVPPDTVRRMMMSGR 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 IYRAAFGVYDPAKGLPDPKNTHTIVSMIAOYTTAAGVSVPPDTVRRMMMSGR 244

OY 245 KGDIMYTGVDGWRKIFRDEGKAFKAGMSNVLRMGAFVLV 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 KATEIIVKNTLHCWATIAKOE-GSAFFKAGAFSNVLRGTGGAFAVLV 288

RESULT 10
O44094 PRELIMINARY: PRT; 288 AA.
ID 044094:
AC 044094:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
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DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE (FRAGMENT).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN (1)
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -I- INNER MEMBRANE (BY SIMILARITY).
CC -I- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF025799; AAB87884.1; -.
DR FlyBase: FBgn0023237; Dsub\sesb.
DR InterPro: IPR001993; Mitoch\_carrier.
DR InterPro: IPR002067; Mit\_carrier.
DR Pfam: PF00153; mito\_cartr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH\_CARRIER. 3.
DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477EB1826 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 4.1e-100;
Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

OY 5 AISFADFLAGIAAISKTAVALPIERVKLLQVHASKOIADKOYKGVDCIVRIPIKE 64
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 7 AIGFVDFDFAAGISAAVSKAVALPIERVKLLQVHISKOISPDKOYKGVDCIVRIPIKE 66

OY 65 QGVLSTWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 124
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 QGFSSTWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 126

OY 125 ATSLCFEYVPLDFARTRLADVGKSGTEREFGGLDCLVITKSDGIRGLYQGFVSVOGI 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 ATSLCFEYVPLDFARTRLADVGKSG- QREFTGLGNCLTKIFKSDGLVGLYRGFVSVOGI 185

OY 185 IYRAAFGVYDPAKGLPDPKNTHTIVSMIAOYTTAAGVSVPPDTVRRMMMSGR 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 IYRAAFGVYDPAKGLPDPKNTHTIVSMIAOYTTAAGVSVPPDTVRRMMMSGR 244

OY 245 KGDIMYTGVDGWRKIFRDEGKAFKAGMSNVLRMGAFVLV 289
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 KATEIIVKNTLHCWATIAKOE-GTAFKAGAFSNVLRGTGGAFAVLV 288

RESULT 11
O25129 PRELIMINARY: PRT; 304 AA.
ID 025129:
AC 025129:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADT/ATP TRANSLOCASE.
GN HRATL1.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN (1)
RP SEQUENCE FROM N.A.
RA Miya T.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
SQ SEQUENCE FROM N.A.
RA Miya T., Makabe K., Satoh N.;
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RT "Expression of a gene for major mitochondrial protein, ADP/ATP
 RT translocase, during embryogenesis in the ascidian *Halocynthia*
 RT roretzi.".
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: D83069; BA01765.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat: Transmembrane; Transport.
 DR SEQUENCE 304 AA; 33306 MW; 51FD0D7DB654880 CRC64;
 SO
 Query Match 76.2%; Score 1176.5; DB 5; Length 304;
 Best Local Similarity 75.8%; Pred. No. 1.9e-99;
 Matches 226; Conservative 20; Mismatches 51; Indels 1; Gaps 1;
 QY 1 MTEQATSPAKDFLAGGIAAISKTAAPLERVKLLQVQHASKOIADKQYGVDCIYR 60
 D6 1 MPMSAVDRAKDLAIGSTAIAISKTIAPLERVKLLQVQVSTQKAGTEYGIIDAIVR 60
 QY 61 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 D6 61 IPKEGVFSLMWGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFVYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 180
 D6 121 GAAGTSLCFVYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 180
 QY 121 GAAGTSLCFVYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 179
 D6 121 GAAGTSLCFVYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 179
 QY 181 VQGITVRAAYGVVDYFAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMM 240
 D6 181 VQGITVRAAYGVVDYFAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMM 240
 QY 180 IQGITVRAAYGVVDYFAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMM 239
 D6 180 IQGITVRAAYGVVDYFAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMM 239
 QY 241 QSGRKADIMYTGIVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 298
 D6 241 QSGRKADIMYTGIVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 298
 QY 240 QSGRKEDRMVYKGVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 297
 D6 240 QSGRKEDRMVYKGVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 297
 RESULT 12
 ID 062526 PRELIMINARY; PRT; 307 AA.
 AC 062526;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANT2 PROTEIN.
 GN ANT2 OR CG1683.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7227;
 RA SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borckova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu N., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jinnai B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RL
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RL Zhang Y.O., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AE003484; AA047956.1; -
 DR EMBL: Y10618; CAF71629.1; -
 DR FlyBase: FBgn0025111; Ant2.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
 DR SEQUENCE 307 AA; 33744 MW; 3D6B3D6D82061C0C CRC64;
 SO
 Query Match 73.7%; Score 1137.5; DB 5; Length 307;
 Best Local Similarity 74.8%; Pred. No. 7.2e-96;
 Matches 217; Conservative 26; Mismatches 46; Indels 1; Gaps 1;
 QY 7 SFAPKFLAGGIAAISKTAAPLERVKLLQVQHASKOIADKQYGVDCIYRIPKDG 66
 D6 7 SFAPKFLAGGIAAISKTAAPLERVKLLQVQHASKOIADKQYGVDCIYRIPKDG 66
 QY 17 SFLPMFMGVSAAIAKTAAPLERVKLLQVQEVSKQIADQKRYGVDCIYRIPKDG 76
 D6 17 SFLPMFMGVSAAIAKTAAPLERVKLLQVQEVSKQIADQKRYGVDCIYRIPKDG 76
 QY 67 VLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 126
 D6 67 VLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 126
 QY 77 FSSFWGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 136
 D6 77 FSSFWGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 136
 QY 127 SLCEFYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 186
 D6 127 SLCEFYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 186
 QY 137 SLCEFYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 195
 D6 137 SLCEFYPLDFARTRLADYKSGTEREPFGDCLVTKTKSDGIRLQYGFVS 195
 QY 187 YRAAFEGVDTAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMMQSGRG 246
 D6 187 YRAAFEGVDTAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMMQSGRG 246
 QY 196 YRAAFEGVDTAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMMQSGRG 255
 D6 196 YRAAFEGVDTAKGLPDKNTHIVSMIAQTVAVAGVSPEDTVRRMMQSGRG 255
 QY 247 ADIMYTGIVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 296
 D6 247 ADIMYTGIVDCMKRIFRDEGKAFFKGSANVLKSGAFVLVLYDELKVI 296
 QY 256 SEMVYKTAHCWLVIAKQEGIAFFKGSANVLKSGAFVLVLYDELKVI 305
 D6 256 SEMVYKTAHCWLVIAKQEGIAFFKGSANVLKSGAFVLVLYDELKVI 305
 RESULT 13
 ID 09H0C2 PRELIMINARY; PRT; 315 AA.
 AC 09H0C2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HYPOTHETICAL 35.0 KDA PROTEIN.
 DKFP434N1235.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Pouscka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AL136857; CAB66791.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mlt_carrier; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 1.
 KW Hypothetical protein; Inner membrane; Mitochondrion; Transmembrane;
 KM Transport. 315 AA; 35022 MW; 9ACE26062CC9675 CRC64;
 SQ SEQUENCE

Query Match 72.5%; Score 1119; DB 4; Length 315;
 Best Local Similarity 72.3%; Pred. No. 3.7e-94;
 Matches 211; Conservative 36; Mismatches 43; Indels 2; Gaps 1;

OY 5 AISFANDLAGGIAAISTKVAPIERVKLLQVQASHAKOIAADKQKIGVDCIVRIPKE 64
 17 ASFGKDLGAGVAAVSTAVAPIERVKLLQVQASHAKOISPEARYKGVDCIVRIPRE 76
 DB 65 QGVLSWRGNLANVIRFTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNLASGGAAG 124
 77 QGFESFWRGNLANVIRFTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNLASGGAAG 136
 DB 125 AATSCFVYPLDFARTPLADVQKSGTEREFGDCLVHTKSDGIRGLYOGFSVVOGI 184
 137 AATSCFVYPLDFARTPLADVQKSGTEREFGDCLVHTKSDGIRGLYOGFSVVOGI 196
 DB 185 IYRAAFVGYDTAKGMLPDKPKNTHIVSMIAQTVTAVAGVSYEPDVTYRRMMQSGR 244
 197 IYRAAFVGYDTAKGMLPDKPKNTHIVSMIAQTVTAVAGVSYEPDVTYRRMMQSGR 256
 DB 245 KQADIVYTGTCVCKRIKIFRDEGKAFKFGAMSNVLRGSGAPLVLYDELKK 296
 257 --AKROYKGLDCEFKRYQHEGISFFRGAFSNVLRGTGALVLYDKIKE 306

RESULT 14
 ID Q21103 PRELIMINARY; PRT: 313 AA.
 AC Q21103;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE KOH12.2 PROTEIN.
 GN KOH12.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurray A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopa A., Saunders D., Shownkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans *.
 RL Nature 368:32-38(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: Z68218; CA92472.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mlt_carrier; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 313 AA; 34384 MW; D1E45DD8463C984 CRC64;

Query Match 67.5%; Score 1041; DB 5; Length 313;
 Best Local Similarity 70.9%; Pred. No. 4.9e-87;
 Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

OY 8 FAKDLAGGIAAISTKVAPIERVKLLQVQASHAKOIAADKQKIGVDCIVRIPKE 67
 25 FLIDLASGAGVAAVSTAVAPIERVKLLQVQASHAKOISPEARYKGVDCIVRIPRE 84
 DB 68 LSPWRGNLANVIRFTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNLASGGAAG 127
 85 AALWRGNLANVIRFTQALNFAFKDKYKQIFLGVDKHTQFRRYRAGNLASGGAAG 144
 DB 128 LCFVYPLDFARTPLADVQKSGTEREFGDCLVHTKSDGIRGLYOGFSVVOGI 187
 145 LCFVYPLDFARTPLADVQKSGTEREFGDCLVHTKSDGIRGLYOGFSVVOGI 203
 DB 188 RAAFVGYDTAKGML-PDKPKNTHIVSMIAQTVTAVAGVSYEPDVTYRRMMQSGR 246
 204 RAAFVGYDTAKGML-PDKPKNTHIVSMIAQTVTAVAGVSYEPDVTYRRMMQSGR 262
 OY 247 ADIMYGTGTCVCKRIKIFRDEGKAFKFGAMSNVLRGSGAPLVLYDELKK 298
 263 -DVLVNTTDCAVKIKINEGSAMFKAUSNVFRGTGALVLYDEIKQFI 313

RESULT 15
 ID P91410 PRELIMINARY; PRT: 313 AA.
 AC P91410;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO ADP/ATP TRANSLOCASE.
 GN T01B11.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopa A., Saunders D., Shownkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Steilyes L.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; 080931; AAB38001.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 KM SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;
 SO

* Query Match 67.3%; Score 1039; DB 5; Length 313;

Best Local Similarity 70.9%; Pred. No. 7.4e-87;
 Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

OY 8 FAKDFLAGGIAAIAISKTAAPIERVKLLQVOHASKOIAADKQYKGIYDCIVIRPEQGV 67
 DB 25 FLIDLASGTAATAVSKTAVAPIERVKLLQVODASLTIAADKRYGIVDLYRVPKEQGY 84
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRIFAGNLASGAAGATS 127
 DB 85 AALMRGNLANVIRYPTQALNFAFKDYKNIFQKGLDKKDFWKFAGNLASGAAGATS 144
 OY 128 LCFVYPLDFARTLAADYKSGTEREFGDCLVKITFKSDGIRGLYOGFSYVOGIITY 187
 DB 145 LCFVYPLDFARTLAADYKKA-NEBEFKGLADCLVKAISDGPITGLYKGFYSVOGIITY 203
 OY 188 RAAVGVYDTAKGML-PPEKNTHTIVSMIAQTVTAAGVVSYPEDTVRRMMOSGRK 246
 DB 204 RAAVGMEDTAKMFTADGKLNFFAAMALAQVTVGSGILSPMDTVRRMMOSGRK- 262
 OY 247 ADIMYTGIVDCNRKIFRDEGKAFKFGANSNLRGMGAFVLYDELKKVI 298
 DB 263 -DVLKNTGLDCAVKIIEKMGSMFKGALSNVFRGTGALVLAIDEIOKFI 313

Search completed: February 13, 2002, 09:34:15
 Job time: 172 sec